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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:17:05 ; Search time 60 seconds
(without alignments)
1290.300 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 1496

Sequence: 1 GSHSLRYSTAVSRGRGEP.....QRYTCHVOHGLPOPLILRW 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1496	100.0	274	4	AAG64618 Human can
2	1496	100.0	362	4	AAG64617 Human can
3	1496	100.0	362	4	ABBS0296 HLA-Cw ov
4	1491	99.7	677	4	ABG26726 Novel hum
5	1311	87.6	271	3	AAB43986 Human can
6	1248	83.4	274	1	AAP80911 Consensus
7	1228	82.1	362	1	AAP70155 Sequence
8	1227	82.1	337	1	AAP70590 Sequence
9	1224	81.8	369	4	AAR12882 Novel hum
10	1209	80.8	366	2	AAR12465 HLA-C exo
11	1206	80.6	366	2	AAY07033 Breast ca
12	1206	80.6	374	4	AAO13073 Human pol
13	1204.5	80.5	374	4	AAO06772 Human pol
14	1201	80.3	362	2	AAR03142 Sequence
15	1200	80.2	362	7	AD64171 Human Pro
16	1200	80.2	362	7	AD64175 Human Pro
17	1199	80.1	362	2	AAR03144 Sequence
18	1199	80.1	366	2	AAR12466 HLA-C exo
19	1192	79.7	380	4	AAR12883 Novel hum
20	1186	79.3	362	2	AAR12464 HLA-B35 a
21	1184	79.1	326	5	AAR12464 HLA-G rec
22	1184	79.1	338	7	ADD46572 Human Pro
23	1182	79.0	362	2	AAR12463 HLA-Bw53
24	1174.5	78.5	379	5	ABP70087 Human NOV
25	1174.5	78.5	379	7	ADE40254 Human NOV

26	1169	78.1	215	4	AAG64619	Aag64619 Human can
27	1162	77.7	368	4	AAM24017	Aam24017 Human NOV
28	1158	77.4	364	5	ABP70088	Abp70088 Human NOV
29	1154	77.1	365	3	AAV68268	Aay68268 Human leu
30	1154	77.1	365	3	AAV52922	Aay52922 HLA-A2/A2
31	1154	77.1	365	4	AAB58683	Aab58683 HLA-A2/A2
32	1154	77.1	365	4	AAB58687	Aab58687 MHC class
33	1153	77.1	280	4	AAU10225	Aau10225 Human leu
34	1153	77.1	280	6	ABU08672	Abu08672 Human his
35	1153	77.1	412	2	AAW68385	Aaw68385 Chimeric
36	1153	77.1	415	4	AAU10224	Aau10224 Human par
37	1153	77.1	415	6	ABU08671	Abu08671 Human sin
38	1153	77.1	510	6	AAE36053	Aae36053 B2M-atacv
39	1151	76.9	365	3	AAV68272	Aay68272 Human leu
40	1151	76.9	365	3	AAV68267	Aay68267 Human leu
41	1151	76.9	365	3	AAV52926	Aay52926 HLA-A2/A2
42	1151	76.9	365	3	AAV52921	Aay52921 HLA-A2/A2
43	1151	76.9	365	4	AAB58682	Aab58682 HLA-A2/A2
44	1151	76.9	365	4	AAB58687	Aab58687 HLA-A2/A2
45	1150	76.9	274	3	AAV68275	Aay68275 Human leu

ALIGNMENTS

RESULT 1

AAG64618
ID AAG64618 standard; protein; 274 AA.

XX AAG64618;

DT 12-SEP-2001 (first entry)

DE Human cancer cell specific HLA-F antigen SEQ ID 5.

KW HLA-F antigen; cancer cell specific; human.

CS Homo sapiens.

XX JP2001095584-A.

XX 10-APR-2001.

XX 30-SEP-1999; 99JP-00279566.

XX 30-SEP-1999; 99JP-00279566.

XX (EGAW/) EGAWA K.

XX (MEDI-) MEDINET KK.

XX (KIMU/) KIMURA K.

XX WPI; 2001-360493/38.

XX N-PSDB; AAH45556.

PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.

XX Claim 2; page 10-11; 12pp; Japanese.

CC This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the invention

XX Sequence 274 AA;

Query Match 100.0%; Score 1496; DB 4; Length 274;

Best Local Similarity 100.0%; Pred. No. 1.3e-133;

Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPREPWVQEQPW 60

Db 1 GSHSLRYFSTAVSRPGRGEPYIAVEYDDTQFLRFDSDAAIPRMEPRPFWVEQGFQYW 60
 Qy 61 EWTGAKANAQTDVALNRLRRYNQSEAGSHTLQMGNGCDMPGDRLLRGYHGHAYDG 120
 Db 61 EWTGAKANAQTDVALNRLRRYNQSEAGSHTLQMGNGCDMPGDRLLRGYHGHAYDG 120
 Qy 121 KDYISLNEEDLSRSTAADTVAQITQRFYEAEBEYAEFRYLGECLELLRRLRYLNGKETLQ 180
 Db 121 KDYISLNEEDLSRSTAADTVAQITQRFYEAEBEYAEFRYLGECLELLRRLRYLNGKETLQ 180
 Qy 181 RADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVTRPAGDGT 240
 Db 181 RADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVTRPAGDGT 240
 Qy 241 FQKWAHVVPVSGEORYTCHVOHEGLPOPLILRW 274
 Db 241 FQKWAHVVPVSGEORYTCHVOHEGLPOPLILRW 274

RESULT 2
 AAG64617
 ID AAG64617 standard; protein; 362 AA.
 AC AAG64617;
 AC AC
 XX XX
 DT 12-SEP-2001 (first entry)
 DE Human cancer cell specific HLA-F antigen SEQ ID 4.
 DE HLA-F antigen; cancer cell specific; human.
 KW Homo sapiens.
 OS Homo sapiens.
 XX JP2001095584-A.
 PN 10-APR-2001.
 PD 30-SEP-1999; 99JP-00279566.
 PF 30-SEP-1999; 99JP-00279566.
 PR 30-SEP-1999; 99JP-00279566.
 XX (EGAW/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 FA (KIMU/) KIMURA K.
 XX WPI; 2001-360493/38.
 DR N-PSDB; AAH45555.
 XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
 XX Disclosure; Page 9-10; 12pp; Japanese.
 PS This invention relates to a cancer cell specific HLA-F antigen. The
 CC invention includes DNA encoding the antigen, and a method for the
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
 CC used in a method to diagnose cancer in which the protein is used to
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
 CC invention represents the cancer cell-specific HLA-F antigen of the
 CC invention
 XX Sequence 362 AA;
 SQ
 Query Match 100.0%; Score 1496; DB 4; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.9e-133;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GSHSLRYFSTAVSRPGRGEPYIAVEYDDTQFLRFDSDAAIPRMEPRPFWVEQGFQYW 60
 Db 22 GSHSLRYFSTAVSRPGRGEPYIAVEYDDTQFLRFDSDAAIPRMEPRPFWVEQGFQYW 81
 Qy 61 EWTGAKANAQTDVALNRLRRYNQSEAGSHTLQMGNGCDMPGDRLLRGYHGHAYDG 120

Db 82 EWTGAKANAQTDVALNRLRRYNQSEAGSHTLQMGNGCDMPGDRLLRGYHGHAYDG 141
 Qy 121 KDYISLNEEDLSRSTAADTVAQITQRFYEAEBEYAEFRYLGECLELLRRLRYLNGKETLQ 180
 Db 142 KDYISLNEEDLSRSTAADTVAQITQRFYEAEBEYAEFRYLGECLELLRRLRYLNGKETLQ 201
 Qy 181 RADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVTRPAGDGT 240
 Db 202 RADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVTRPAGDGT 261
 Qy 241 FQKWAHVVPVSGEORYTCHVOHEGLPOPLILRW 274
 Db 262 FQKWAHVVPVSGEORYTCHVOHEGLPOPLILRW 295

RESULT 3
 ABB50296
 ID ABB50296 standard; protein; 362 AA.
 AC ABB50296;
 AC AC
 XX XX
 DT 08-FEB-2002 (first entry)
 DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.
 DE Ovarian tumour marker gene; human; overexpression; upregulation;
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
 KW identification; serous cystadenoma; borderline serous tumour;
 KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
 KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
 KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
 KW adenofofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
 KW immune response pathway; cell proliferation regulation; protein folding;
 KW membrane localised; secreted; therapeutic target; cytostatic;
 KW gene therapy; vaccine.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200175177-A2.
 PN 11-OCT-2001.
 PD 03-APR-2001; 2001WO-US010947.
 PF 03-APR-2000; 2000US-0194336P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
 XX WPI; 2001-626450/72.
 DR N-PSDB; ABA83122.
 XX Detecting and identifying ovarian tumor, identifying increased risk for
 PT developing ovarian cancer, and determining effectiveness of ovarian
 PT cancer treatment, by measuring expression level of ovarian tumor marker
 PT gene.
 XX Claim 23; Page 126-127; 140pp; English.
 PS The invention relates to methods for diagnosing and prognosing ovarian
 CC tumours in an individual via the detection and measurement of the
 CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183). The methods of the invention are useful for
 CC detecting an ovarian tumour in a patient, for identifying an individual
 CC at increased risk for developing ovarian cancer, in prognostic tests for
 CC assessing the relative severity of ovarian cancer, in tests for
 CC monitoring a patient in remission from ovarian cancer and in tests for
 CC monitoring disease status in a patient being treated for ovarian cancer.
 CC The methods can additionally be used to identify a particular tumour as
 CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,

CC mucinous cystadenoma, borderline mucinous tumour, mucinous
CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
CC tumour. The ovarian tumour marker genes of the invention were identified
CC using SAGE (serial analysis of gene expression) and were found to be
CC overexpressed in a broad variety of ovarian epithelial tumour cells
CC relative to normal ovarian epithelial cells. The marker genes are
CC implicated in immune response pathways, in the regulation of cell
CC proliferation and in protein folding, and many of these are membrane-
CC localised or secreted. In addition to their use as diagnostic and
CC prognostic markers, the ovarian tumour marker genes or their encoded
CC proteins may be used as therapeutic targets for the treatment and
CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent
CC proteins encoded by ovarian tumour marker genes of the invention
XX
SQ Sequence 362 AA;

Query Match 100.0%; Score 1496; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.9e-133;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 60
Db 22 GSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 81

QY 61 EWTGAKANAQDRVALNRLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 120
Db 82 EWTGAKANAQDRVALNRLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 141

QY 121 KDYISLNEDLSRSTAADTVAQITQRYEAEYAEFFRYLGECELELLRRLYENGKETLQ 180
Db 142 KDYISLNEDLSRSTAADTVAQITQRYEAEYAEFFRYLGECELELLRRLYENGKETLQ 201

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLVETRPAGDGT 240
Db 202 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLVETRPAGDGT 261

QY 241 FQKAAVVPVSGEORYTCHVQHEGLPQPLILRW 274
Db 262 FQKAAVVPVSGEORYTCHVQHEGLPQPLILRW 295

RESULT 4
ABG26726
ID ABG26726 standard; protein; 677 AA.
XX
AC ABG26726;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #26717.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
PI WPI; 2001-639362/73.
XX
DR N-PSDB; AAS90913.
XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 57085; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 677 AA;

Query Match 99.7%; Score 1491; DB 4; Length 677;
Best Local Similarity 99.6%; Pred. No. 1.3e-132;
Matches 273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 60
Db 331 GSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 390

QY 61 EWTGAKANAQDRVALNRLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 120
Db 391 EWTGAKANAQDRVALNRLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 450

QY 121 KDYISLNEDLSRSTAADTVAQITQRYEAEYAEFFRYLGECELELLRRLYENGKETLQ 180
Db 451 KDYISLNEDLSRSTAADTVAQITQRYEAEYAEFFRYLGECELELLRRLYENGKETLQ 510

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLVETRPAGDGT 240
Db 511 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLVETRPAGDGT 570

QY 241 FQKAAVVPVSGEORYTCHVQHEGLPQPLILRW 274
Db 571 FQKAAVVPVSGEORYTCHVQHEGLPQPLILRW 604

RESULT 5
AAB43986
ID AAB43986 standard; protein; 271 AA.
XX
AC AAB43986;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated protein sequence SEQ ID NO:1431.
XX
KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnarary; immunomodulator;
KW antidiabetic; antiasthmatic; antineumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;

KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.

XX Homo sapiens.
XX WO20005350-A1.
XX 21-SEP-2000.
XX 08-MAR-2000; 2000WO-US005882.
XX 12-MAR-1999; 99US-0124270P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2000-587533/55.
XX N-PSDB; AAC78195.
XX Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer.
XX Claim 11; Page 2115-2116; 2352pp; English.
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in
XX AAB43398 to AAB44239. The proteins can have activities based on the
XX tissues and cells the genes are expressed in. Example of activities
XX include: cytostatic; proliferative; vulnary; immunomodulatory;
XX antidiabetic; antiaesthetic; antirheumatic; antithrombotic;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
XX dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
XX notropic; vasotropic; antipsoriatic and antiangiogenic. The
XX polynucleotides and polypeptides can be used for preventing, treating or
XX ameliorating medical conditions and diagnosing pathological conditions.
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from
XX the present invention may be used to treat immune disorders by activating
XX or inhibiting the proliferation, differentiation or mobilisation of
XX immune cells, to treat disorders of haematopoietic cells, autoimmune
XX disorders, allergic reactions, graft versus host disease and organ
XX rejection, modulate haemostatic or thrombolytic activity, modulate
XX inflammation, cancers, cardiovascular disorders, neurological disease and
XX bacterial or viral infections. The peptides, nucleotides, antibodies,
XX agonists and antagonists may be also be used in drug screens. AAC78449 to
XX AAC78457 and AAB44240 represent sequences used in the exemplification of
XX the present invention

XX Sequence 271 AA;
Query Match 87.6%; Score 1311; DB 3; Length 271;
Best Local Similarity 99.6%; Pred. No. 4.8e-116;
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 60
DB 28 GSHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 87
QY 61 EWTGAKANAQTDRAVALNRLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAYDG 120
DB 88 EWTGAKANAQTDRAVALNRLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAYDG 147
QY 121 KDYISLNEDLRSWTAADTVAQITQRFYAEAEYAEFPYILEGECLELLRRYLENGKETLQ 180
DB 148 KDYISLNEDLRSWTAADTVAQITQRFYAEAEYAEFPYILEGECLELLRRYLENGKETLQ 207
QY 181 RADPKARVAHPISDHEATLRCAWLGYPAEITLTWQDGEQOTQELVETRPAGDGT 240
DB 208 RADPKARVAHPISDHEATLRCAWLGYPAEITLTWQDGEQOTQELVETRPAGDGT 267
QY 241 FQ 242
DB 268 PR 269

XX Result 6
AAP80911
ID AAP80911 standard; protein; 274 AA.
XX AAP80911;
AC AAP80911;
XX 25-MAR-2003 (revised)
DT 18-SEP-1990 (first entry)
XX Consensus sequence of peptides which constitute the alpha-1, alpha-2 and
DE alpha-3 regions of a class I HLA molecule.
XX HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1..90
FT /note= "alpha-1 region"
FT 91..180
FT /note= "alpha-2 region"
FT 181..272
FT /note= "alpha-3 region"
XX WO8905784-A.
PN 11-AUG-1988.
XX 27-JAN-1988; 88WO-US000245.
PR 30-JAN-1987; 87US-00008846.
PR 24-DEC-1987; 87US-00138547.
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX Krensky AM, Parham P, Clayberger C;
XX WPI; 1988-235147/33.
XX New peptide corresp. to major histocompatibility antigen regions - used
PT for modulating cytotoxic T-lymphocyte activity in e.g. transplants or
PT auto-immune diseases.
XX Example 9; Fig 4; 60pp; English.
XX The consensus sequence is derived from a total of 23 HLA-A,B,C sequences.
CC The protein sequences in the three extracellular domains (alpha-1, alpha-
CC 2 and alpha-3) are shown. The example concerned the effect of peptides
CC from different HLA-A2 epitopes on cytotoxicity of target cells by CTL of
CC different specificities. (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX Sequence 274 AA;
Query Match 83.4%; Score 1248; DB 1; Length 274;
Best Local Similarity 82.8%; Pred. No. 4.8e-110;
Matches 227; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 60
DB 1 GSHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 60
QY 61 EWTGAKANAQTDRAVALNRLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAYDG 120
DB 61 DRETQVKAQSDTDRDLTLLRGYHQAYDG 120
QY 121 KDYISLNEDLRSWTAADTVAQITQRFYAEAEYAEFPYILEGECLELLRRYLENGKETLQ 180
DB 121 KDYISLNEDLRSWTAADTVAQITQRFYAEAEYAEFPYILEGECLELLRRYLENGKETLQ 180

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTQDTVELVETRPAGDGT 240
DB 181 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQTDQDTVELVETRPAGDGT 240
QY 241 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 274
DB 241 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 274

RESULT 7
AAP70155
ID AAP70155 standard; protein; 362 AA.
XX AC AAP70155;
XX DT 25-MAR-2003 (revised)
XX DT 10-MAR-1993 (revised)
XX DT 03-APR-1991 (first entry)
XX
XX Sequence encoded by genomic DNA encoding human histocompatibility antigen
XX HLA-B 27.
XX DE
XX DE
XX KW Ankylosing spondylitis; rheumatic disorder; diagnosis.
XX XX
XX OS Homo sapiens.
XX PN
XX PN EP226069-A.
XX PD
XX PD 24-JUN-1987.
XX PF 21-NOV-1986; 86EP-00116139.
XX PR 30-NOV-1985; 85DE-00542024.
XX PR 21-DEC-1985; 85DE-03545576.
XX PA (BEHW) BEHRINGWERKE AG.
XX PI Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G;
XX WPI; 1987-171469/25.
XX DR N-PSDB; AAN70225.
XX
XX DNA coding for human histocompatibility antigen HLA-B 27 - useful for
XX diagnosis and antigen and antibody prodn.
XX PT
XX PS Disclosure; Page 6; 13pp; German.
XX
XX The DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human
XX genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27
XX antibodies in human serum. The antibodies may be used to determine HLA-B
XX 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp.
XX ankylosing spondylitis. (Updated on 25-MAR-2003 to correct PR field.)
XX SQ
XX Sequence 362 AA;
Query Match 82.1%; Score 1228; DB 1; Length 362;
Best Local Similarity 82.1%; Pred. No. 5 6e-108;
Matches 225; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
DB 25 GSHSMRYFHTSVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 84
QY 61 EWTTCYAKANAOTDRVALNLLRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAIDG 120
DB 85 DRETQICKAKAQTDREDLRTLLRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAIDG 144
QY 121 KDYISLNEDLSRWTAAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRYLENGKETLQ 180
DB 145 KDYIALNEDLSWTAAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRYLENGKETLQ 204
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTQDTVELVETRPAGDGT 240

DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTQDTVELVETRPAGDRT 264
QY 241 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 274
DB 265 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298

RESULT 8
AAP70590
ID AAP70590 standard; protein; 337 AA.
XX AC AAP70590;
XX DT 10-APR-1991 (first entry)
XX DE
XX DE Sequence of the human histocompatibility antigen HLA B27.
XX KW Rheumatic disorder; genetic screening; diagnosis; ankylosing spondylitis.
XX XX
XX OS Homo sapiens.
XX PN DE3542024-A.
XX PD 04-JUN-1987.
XX PF 28-NOV-1985; 85DE-03542024.
XX PR 21-DEC-1985; 85DE-03545576.
XX PA (BEHW) BEHRINGWERKE AG.
XX PI Riethmuller G, Meo T, Weiss E, Szots H;
XX WPI; 1987-157893/23.
XX DR N-PSDB; AAN70935.
XX PT
XX PT DNA coding for antigen HLA B27 - and diagnostic reagents contg. such DNA,
XX antigen or antibody.
XX PS Disclosure; Page 5; 5pp; German.
XX
XX The DNA may be used as a hybridisation probe for detecting the HLA B27
XX gene, eg for assessing susceptibility to rheumatic disorders such as
XX ankylosing spondylitis, or may be used to transform cells for prodn. of
XX HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human
XX serum, or to produce mono- or polyclonal HLA B27 antibodies for use in
XX immunoassay
XX SQ
XX Sequence 337 AA;
Query Match 82.1%; Score 1227.5; DB 1; Length 337;
Best Local Similarity 82.5%; Pred. No. 5.7e-108;
Matches 226; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
DB 1 GSHSMRYFHTSVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
QY 61 EWTTCYAKANAOTDRVALNLLRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAIDG 120
DB 61 DRETQICKAKAQTDREDLRTLLRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAIDG 119
QY 121 KDYISLNEDLSRWTAAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRYLENGKETLQ 180
DB 120 KDYIALNEDLSWTAAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRYLENGKETLQ 179
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTQDTVELVETRPAGDGT 240
DB 180 RVDPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTQDTVELVETRPAGDRT 239
QY 241 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 274
DB 240 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 273

RESULT 9
 AAU32882
 ID AAU32882 standard; protein; 369 AA.
 XX
 AC
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #3373.
 XX
 DE Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 XX
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-611725/70.
 XX
 DR Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 PS Claim 20; Page 683; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 SQ Sequence 369 AA;
 Query Match 81.8%; Score 1224; DB 4; Length 369;
 Best Local Similarity 81.0%; Pred. No. 1.4e-107;
 Matches 222; Conservative 21; Mismatches 31; Indels 0; Gaps 0;
 QY 1 GSHSLRYPSTAVSRGGRGPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPFWBQEGPQYW 60
 DB 28 GSHSNRYPDPTAMSRGGRGPRFISVGYVDDTQFLRFDSDAASPRPFWBQEGPQYW 87
 QY 61 EWTGYAKANAQTDRLVALNRLRRYNYQSEAGSHTLQGMGCDMGPDGRLRLRGVHQHAYDG 120
 DB 88 DRNTQIFKNTQTDRSLRNRLRGYNYQSEAGSHTLQSMYGDVDPDGLLGNHNYAYDG 147
 QY 121 KDYISLNEEDLSRWTAAADTVAQITQRFYAEYAEFEFTYLEGECLELLRRLYLENGKSTLQ 180
 DB 148 KDYIALNEDLSRWTAAADTAAQITQKWEAARVAEODRAYLEGTVCVRLRYLENGKSTLE 207

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQOTDTTELVTETRPAGDGT 240
 DB 208 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEQOTDTTELVTETRPAGDRT 267
 QY 241 FOKWAAVVVPSGEGQRVTCHVQHEGLPQPLILRW 274
 DB 268 FOKWAAVVVPSGEGQRVTCHVQHEGLPQPLILRW 301
 RESULT 10
 AAU12465
 ID AAU12465 standard; protein; 366 AA.
 XX
 AC AAU12465;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-AUG-1991 (first entry)
 XX
 DE HLA-C exon Cb-1.
 XX
 KW Human leukocyte antigen; probe; major histocompatibility complex; MHC;
 KW class I.
 XX
 OS Homo sapiens.
 XX
 PN JP03112485-A.
 XX
 PD 14-MAY-1991.
 XX
 PF 22-SEP-1989; 89JP-00247695.
 XX
 PR 22-SEP-1989; 89JP-00247695.
 XX
 PA (OLYU) OLYMPUS OPTICAL CO LTD.
 XX
 DR WPI; 1991-182989/25.
 DR N-PSDB; AAQ12116.
 XX
 PT HLA-C gene, DNA probe and transformant cells - for immunisation of
 PT animals and monoclonal antibody development.
 XX
 PS Claim 3; Page 2; 13pp; Japanese.
 XX
 CC Probes comprising part of the DNA sequence encoding the protein can be
 CC used to identify Class I genes. The DNA can be expressed for immunisation
 CC of animals and prodn. of monoclonal antibodies specific for the HLA-C
 CC antigen. See also AAU12466 (same patent) and J03112486 and J03112487.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 366 AA;
 Query Match 80.8%; Score 1209; DB 2; Length 366;
 Best Local Similarity 81.7%; Pred. No. 3.7e-106;
 Matches 223; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
 QY 2 SHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPFWBQEGPQYWE 61
 DB 26 SHSMRYFSTSVSRGGRGPRFIAVGVDVTQFLRFDSDAASPRGPRAPFWBQEGPEYWD 85
 QY 62 WTTGYAKANAQTDRLVALNRLRRYNYQSEAGSHTLQGMGCDMGPDGRLRLRGVHQHAYDGK 121
 DB 86 RETQKYRCAQTDRLVSLNRLRGYNYQSEAGSHTLQWFGCDLGPGRLLRGVYDQSAIDGK 145
 QY 122 DYISLNEEDLSRWTAAADTVAQITQRFYAEYAEFEFTYLEGECLELLRRLYLENGKSTLQ 181
 DB 146 DYIALNEDLSRWTAAADTAAQITQKWEAARVAEODRAYLEGTVCVRLRYLENGKSTLQ 205
 QY 182 ADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQOTDTTELVTETRPAGDGT 241
 DB 206 AEPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQDGEDTQDTTELVTETRPAGDGT 265
 QY 242 QKWAADVVPSSGEGQRVTCHVQHEGLPQPLILRW 274

QY 2 SHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYWE 61
DB 34 SHSNRYFYTTAVSRGGEPRFIAGVYVDDTQFVRFDSDAASPRGEPRAAPWVEQGEPEYWD 93
QY 62 WTTGYAKANAQTRVALNRLRRYNOSEAGSHTLQMGNGCDMGDPDGRLLRGYHQAIDGK 121
DB 94 RETQYKROQOTRVSRLNLRGYNQSEAGSHTLQMGNGCDLPGDGLRLGVDQSAIDGK 153
QY 122 DYISLNEEDLSWTAADTVAQITQFYEAEBYAEFRYLEGECELELRLRYLENGKETLQ 181
DB 154 DYIALNEHLSCTAADAATAAQITQKWEAARAABQWRAYLEGTCVWLRLRYLENGKETLQ 213
QY 182 ADPPKAVVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEBOFOTDELVELVETRPAGDGT 241
DB 214 AEPKTKVTHHPVSDHEATLRCWALGFYPAEITLTWQDGEDQTDDELVELVETRPAGDGT 273
QY 242 QKWAUVVPSGGEQRYTCHVQHEGLPOPLIRW 274
DB 274 QKWAUVVPSGGEQRYTCHVQHEGLPEPLIRW 306

RESULT 13
AAO06772
ID AAO06772 standard; protein; 374 AA.

AC AAO06772;
XX
XX 06-NOV-2001 (first entry)
XX Human polypeptide SEQ ID NO 20664.
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX Homo sapiens.
XX WO200164835-A2.
XX
PD 07-SEP-2001.
XX 26-FEB-2001; 2001WO-US004927.
XX 28-FEB-2000; 2000US-00515126.
XX 18-MAY-2000; 2000US-00577409.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX N-PSDB; AAI86703.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 20664; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIFO at fcp.wifo.int/pub/published_pct_sequences

SQ Sequence 374 AA;
Query Match 80.5%; Score 1204.5; DB 4; Length 374;
Best Local Similarity 81.8%; Pred. No. 1e-105;
Matches 225; Conservative 15; Mismatches 34; Indels 1; Gaps 1;
QY 1 GSHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYWE 60
DB 25 GSHSNRYFYTTAVSRGGEPRFIAGVYVDDTQFVRFDSDAASPRGEPRAAPWVEQGEPEYW 84
QY 61 EWTTGYAKANAQTRVALNRLRRYNOSEAGSHTLQMGNGCDMGDPDGRLLRGYHQAIDGK 120
DB 85 DRETRNMKASQAQTYRENLRIRALRYNOSEAGSHTLQRMYGCDVPGDGLRLRGYHQAIDGK 144
QY 121 KDYISLNEEDLSWTAADTVAQITQFYEAEBYAEFRYLEGECELELRLRYLENGKETLQ 180
DB 145 KDYIALNEEDLSWTAADTAAQITQKWEAARAABQWRAYLEGTCVWLRLRYLENGKETLQ 204
QY 181 RADPPKAVVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEBOFOTDELVELVETRPAGDGT 240
DB 205 RADPPKTKVTHHPVSDHEATLRCWALGFYPAEITLTWQDGEDQTDDELVELVETRPAGDGT 264
QY 241 FOKWAUVVPSGGEQRYTCHVQHEGLPOPLI-LRW 274
DB 265 FOKWAUVVPSGGEQRYTCHVQHEGLPKPLTPERW 299

RESULT 14
AAR03142
ID AAR03142 standard; protein; 362 AA.

XX AAR03142;
XX AC AAR03142;
XX 25-MAR-2003 (revised)
XX 19-MAR-1991 (first entry)
XX Sequence of HLA-Bw52 antigen.
XX DE
XX KW Probe; HLA class I DNA; immunogen.
XX OS Homo sapiens.
XX PN BP354580-A.
XX PD 14-FEB-1990.
XX PF 10-AUG-1989; 89EP-00114857.
XX PR 11-AUG-1988; 88JP-00200758.
XX (OLYU) OLYMPUS OPTICAL CO LTD.
XX Kano K, Takiguchi M;
XX WPI; 1990-046289/07.
XX New DNA for class 1 human leucocyte antigens - with derived probes and
XX transformed cells, used for DNA typing, as immunogens etc.
XX Disclosure; Page 13; 23pp; English.

XX The HLA class I DNA can be used as a source of probes for use in DNA typing.
XX transformed cells, which are useful as immunogens, can be obtained by
XX CC introducing these DNAs into eucaryotic cells. (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX SQ Sequence 362 AA;

Query Match 80.3%; Score 1201; DB 2; Length 362;
Best Local Similarity 80.3%; Pred. No. 2.1e-105;
Matches 220; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYWE 60

Db 25 GSHSMRYFTAMSRPGRGPRFIAVGYDDTQVRFDSDAASPRTEPRAPWIEQGEPEY 84
QY 61 EWTGYAKANAQTRVALNRLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDG 120
Db 85 DRETQSKNTQTYRENLRALRYNQSEAGSHTWQMTYGCDDVGPGRLLRGHNOYAYDG 144
QY 121 KDYSISNEDLRSTAAADTVAQITQRYEAEVEEFTYLEGECLELLRYLNGKETLQ 180
Db 145 KDYIALNEDLSSTAAADTAAQITQKWEAREAEQURAYDEGLCVBWLRRHLENGKETLQ 204
QY 181 RADPPKHAHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEPRAGDGT 240
Db 205 RADPPKTHVTHPVSDEATLRCWALGFYPAEITLTWQDGEQTDTELVEPRAGDRT 264
QY 241 FQKWAADVVPSEGEORYTCHVQHEGLPOPLILRW 274
Db 265 FQKWAADVVPSEGEORYTCHVQHEGLPKPLILRW 298

RESULT 15
ADE64171
ID ADE64171 standard; protein; 362 AA.
XX ADE64171;
XX DT 29-JAN-2004 (first entry)
XX Human Protein P30474, SEQ ID NO 10123.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX W02003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-269312/26.
DR GENBANK; P30474.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 362 AA;
Query Match 80.2%; Score 1200; DB 7; Length 362;
Best Local Similarity 80.3%; Pred. No. 2.6e-105;
Matches 220; Conservative 18; Mismatches 36; Indels 0; Gaps 0;
QY 1 GSHSLRYESTAVSRPGRGPRYIAVEYDDTQFLRFDSDAAI PRMEPREPWVEQGPQY 60
Db 25 GSHSMRYFTAMSRPGRGPRFIAVGYDDTQVRFDSDAASPRTEPRAPWIEQGEPEY 84
QY 61 EWTGYAKANAQTRVALNRLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDG 120
Db 85 DRETQSKNTQTYRENLRALRYNQSEAGSHTWQMTYGCDDVGPGRLLRGHNOYAYDG 144
QY 121 KDYSISNEDLRSTAAADTVAQITQRYEAEVEEFTYLEGECLELLRYLNGKETLQ 180
Db 145 KDYIALNEDLSSTAAADTAAQITQKWEAREAEQURAYDEGLCVBWLRRHLENGKETLQ 204
QY 181 RADPPKHAHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEPRAGDGT 240
Db 205 RADPPKTHVTHPVSDEATLRCWALGFYPAEITLTWQDGEQTDTELVEPRAGDRT 264
QY 241 FQKWAADVVPSEGEORYTCHVQHEGLPOPLILRW 274
Db 265 FQKWAADVVPSEGEORYTCHVQHEGLPKPLILRW 298

Search completed: June 18, 2004, 19:21:12
Job time : 63 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:28:42 ; Search time 22 Seconds
(without alignments)
642.978 Million cell updates/sec

Title: US-09-819-371-5
Perfect score: 274
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Scoring table: OLIGO
Gapop 60.0 , Gapext 50.0

Searched: 389414 seqs, 51625971 residues

Word size : 0
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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5: /cgn2_6/prodata/2/iaa/PCITUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	16.1	274	1	US-08-222-851-1
2	39	14.2	117	2	US-08-406-057-9
3	39	14.2	117	3	US-08-958-316-9
4	39	14.2	117	2	US-08-406-057-8
5	39	14.2	145	3	US-08-358-316-8
6	30	10.9	289	2	US-08-484-905-79
7	30	10.9	289	3	US-08-481-985B-79
8	30	10.9	289	3	US-08-370-476-79
9	29	10.6	274	2	US-08-484-905-105
10	29	10.6	274	2	US-08-484-905-107
11	29	10.6	274	2	US-08-484-905-108
12	29	10.6	274	3	US-08-481-985B-105
13	29	10.6	274	3	US-08-481-985B-107
14	29	10.6	274	3	US-08-481-985B-108
15	29	10.6	274	3	US-08-370-476-105
16	29	10.6	274	3	US-08-370-476-107
17	29	10.6	274	3	US-08-370-476-108
18	29	10.6	341	3	US-08-890-719-38
19	29	10.6	365	2	US-08-484-905-97
20	29	10.6	365	2	US-08-484-905-98
21	29	10.6	365	2	US-08-484-905-99
22	29	10.6	365	2	US-08-484-905-100
23	29	10.6	365	2	US-08-484-905-101
24	29	10.6	365	3	US-08-481-985B-97
25	29	10.6	365	3	US-08-481-985B-98
26	29	10.6	365	3	US-08-481-985B-99
27	29	10.6	365	3	US-08-481-985B-100

28	29	10.6	365	3	US-08-481-985B-101	Sequence 101, Appl
29	29	10.6	365	3	US-08-652-265-23	Sequence 23, Appl
30	29	10.6	365	3	US-08-834-437A-23	Sequence 23, Appl
31	29	10.6	365	3	US-08-370-476-97	Sequence 97, Appl
32	29	10.6	365	3	US-08-370-476-98	Sequence 98, Appl
33	29	10.6	365	3	US-08-370-476-99	Sequence 99, Appl
34	29	10.6	365	3	US-08-370-476-100	Sequence 100, Appl
35	29	10.6	365	3	US-08-370-476-101	Sequence 101, Appl
36	29	10.6	365	3	US-09-503-444A-23	Sequence 23, Appl
37	27	9.9	184	2	US-08-484-905-83	Sequence 83, Appl
38	27	9.9	184	3	US-08-481-985B-83	Sequence 83, Appl
39	27	9.9	184	3	US-08-370-476-83	Sequence 83, Appl
40	25	9.1	108	2	US-08-484-905-82	Sequence 82, Appl
41	25	9.1	108	3	US-08-481-985B-82	Sequence 82, Appl
42	25	9.1	108	3	US-08-370-476-82	Sequence 82, Appl
43	25	9.1	290	2	US-08-484-905-80	Sequence 80, Appl
44	25	9.1	290	3	US-08-481-985B-80	Sequence 80, Appl
45	25	9.1	290	3	US-08-370-476-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KEENSKY, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222.851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRNFOERSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-222-851-1

Query Match 16.1%; Score 44; DB 1; Length 274;
Best Local Similarity 100.0%; Pred.No. 1.2e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTVELVETPAGDGTQKNAVVVPSGEGQRYTCHVQHEGLP 267
DB 224 QTQDTVELVETPAGDGTQKNAVVVPSGEGQRYTCHVQHEGLP 267

RESULT 2
US-08-406-057-9
; Sequence 9, Application US/08406057
; Patent No. 5856442
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 03179
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 846-331-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-057-9

Query Match 14.2%; Score 39; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267
|||||
Db 51 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 89
|||||

RESULT 3
US-08-958-316-9
; Sequence 9, Application US/08958316
; Patent No. 6291659
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 27-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0846-0437-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-958-316-9

Query Match 14.2%; Score 39; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267
|||||
Db 51 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 89
|||||

RESULT 4
US-08-406-057-8
; Sequence 8, Application US/08406057
; Patent No. 5856442
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 03179

;; FILING DATE: 18-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NORMAN F
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 846-331-0
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 413-3000
;; TELEFAX: (703) 413-2220
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 145 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
US-08-406-057-8

Query Match 14.2%; Score 39; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHGGLP 267
Db 79 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHGGLP 117

RESULT 5
US-08-958-316-8
; Sequence 8, Application US/08958316
; Patent No. 6291659
; GENERAL INFORMATION:
; APPLICANT: CARSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,316
; FILING DATE: 27-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 03179
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0846-0437-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-958-316-8
Query Match 14.2%; Score 39; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 229 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHGGLP 267
Db 79 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHGGLP 117
RESULT 6
US-08-484-905-79
; Sequence 79, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-905-79

Query Match 10.9%; Score 30; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 9.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 QDELVETRPAGDGTFOKWAAVVPSGEEQ 255
Db 226 QDELVETRPAGDGTFOKWAAVVPSGEEQ 255

RESULT 7
US-08-481-985B-79

Sequence 79, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-79

Query Match 10.9%; Score 30; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 9.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 QDTELVTETPAGDGTFOKWAAVVPSGEQ 255
Db 226 QDTELVTETPAGDGTFOKWAAVVPSGEQ 255

RESULT 8
US-08-370-476-79
Sequence 79, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Casrouge, Armand
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-79

Query Match 10.9%; Score 30; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 9.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 QDTELVTETPAGDGTFOKWAAVVPSGEQ 255
Db 226 QDTELVTETPAGDGTFOKWAAVVPSGEQ 255

RESULT 9
US-08-484-905-105
Sequence 105, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-105

Query Match 10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTLTVETRPAGDGTQKWAADVVPSSG 252
Db 224 QTQDTLTVETRPAGDGTQKWAADVVPSSG 252

RESULT 10
US-08-484-905-107
Sequence 107, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-107

Query Match 10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTLTVETRPAGDGTQKWAADVVPSSG 252
Db 224 QTQDTLTVETRPAGDGTQKWAADVVPSSG 252

RESULT 11
US-08-484-905-108
Sequence 108, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-108

```
Query Match      10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252
Db 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252

RESULT 12
US-08-481-985B-105
; Sequence 105, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-105

Query Match      10.6%; Score 29; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252
Db 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252

RESULT 13
US-08-481-985B-107
; Sequence 107, Application US/08481985B
; Patent No. 6011146
```

```
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-107

Query Match      10.6%; Score 29; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252
Db 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252

RESULT 14
US-08-481-985B-108
; Sequence 108, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-108

Query Match 10.6%; Score 29; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKWAAVVPSG 252
DB 224 QTQDTLVETRPAGDGTFOKWAAVVPSG 252

RESULT 15
US-08-370-476-105
Sequence 105, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lome, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Carrouge, Armand
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575

FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-105

Query Match 10.6%; Score 29; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKWAAVVPSG 252
DB 224 QTQDTLVETRPAGDGTFOKWAAVVPSG 252

Search completed: June 18, 2004, 19:32:29
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:25:36 ; Search time 22 Seconds
(without alignments)
642.978 Million cell updates/sec

Title: US-09-819-371-5
Perfect score: 1496
Sequence: 1 GSHSLRYFSTAVSRGEPRIAYVEYDDTQFLRFDSDAAI PRMEPRFPWQEPQYW 274

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1248	83.4	274	1	US-08-222-851-1
2	1154	77.1	365	2	US-08-484-905-100
3	1154	77.1	365	3	US-08-481-985B-100
4	1154	77.1	365	3	US-08-652-265-23
5	1154	77.1	365	3	US-08-834-497A-23
6	1154	77.1	365	3	US-08-370-476-100
7	1154	77.1	365	3	US-08-503-444A-23
8	1153	77.1	341	3	US-08-890-719-38
9	1151	76.9	365	2	US-08-484-905-99
10	1151	76.9	365	2	US-08-484-905-104
11	1151	76.9	365	3	US-08-481-985B-99
12	1151	76.9	365	3	US-08-481-985B-104
13	1151	76.9	365	3	US-08-370-476-99
14	1151	76.9	365	3	US-08-370-476-104
15	1150	76.9	274	2	US-08-484-905-107
16	1150	76.9	274	2	US-08-484-905-108
17	1150	76.9	274	3	US-08-481-985B-107
18	1150	76.9	274	3	US-08-481-985B-108
19	1150	76.9	274	3	US-08-370-476-107
20	1150	76.9	274	3	US-08-370-476-108
21	1147	76.7	365	2	US-08-484-905-97
22	1147	76.7	365	2	US-08-484-905-98
23	1147	76.7	365	3	US-08-481-985B-97
24	1147	76.7	365	3	US-08-481-985B-98
25	1147	76.7	365	3	US-08-370-476-97
26	1147	76.7	365	3	US-08-370-476-98
27	1146	76.6	274	2	US-08-484-905-105

28	1146	76.6	274	3	US-08-481-985B-105	Sequence 105, App
29	1146	76.6	274	3	US-08-370-476-105	Sequence 105, App
30	1142	76.3	274	2	US-08-484-905-106	Sequence 106, App
31	1142	76.3	274	3	US-08-481-985B-106	Sequence 106, App
32	1142	76.3	274	3	US-08-370-476-106	Sequence 106, App
33	1142	76.3	365	2	US-08-484-905-103	Sequence 103, App
34	1142	76.3	365	3	US-08-481-985B-103	Sequence 103, App
35	1142	76.3	365	3	US-08-370-476-103	Sequence 103, App
36	1141	76.3	365	2	US-08-484-905-102	Sequence 102, App
37	1141	76.3	365	3	US-08-481-985B-102	Sequence 102, App
38	1141	76.3	365	3	US-08-370-476-102	Sequence 102, App
39	1133	75.7	365	2	US-08-484-905-101	Sequence 101, App
40	1133	75.7	365	3	US-08-481-985B-101	Sequence 101, App
41	1133	75.7	365	3	US-08-370-476-101	Sequence 101, App
42	1097	73.3	361	3	US-08-652-265-22	Sequence 22, Appl
43	1097	73.3	361	3	US-08-834-497A-22	Sequence 22, Appl
44	1097	73.3	361	3	US-09-503-444A-22	Sequence 22, Appl
45	1071	71.6	361	4	US-08-914-372C-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRNFORSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-222-851-1

Query Match 83.4%; Score 1248; DB 1; Length 274;
Best Local Similarity 82.6%; Pred. No. 4.3e-114;
Matches 227; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGEPRIAYVEYDDTQFLRFDSDAAI PRMEPRFPWQEPQYW 60
DB 1 GSHSMYFTYSVRGEPRIAYGYDDTQFLRFDSDAASPRMEPRAPWIEQEPQYW 60

Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLYFSTAVSRPGGEPRIYAVYDDTQFLRFDSDAAIPRMEPRPWPVEGPOYW 60
DB 25 GSHSMRYFSTSVSRPGGEPRIYAVYDDTQFLRFDSDAAIPRMEPRPWPVEGPOYW 84
QY 61 EMTTGYAKANAQDRVALNLLRRYNOSEAGSHTLQGMNGCDMPDGRLLRGVHQHAYDG 120
DB 85 DGETRKVKAHQTHRVLDLTLRGVYNOSEAGSHTLQGMNGCDMPDGRLLRGVHQHAYDG 144
QY 121 KDYISLNEDLSRWTAAADTVAQITQFYEAEBEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
DB 145 KDYIALKEDLSRWTAAADTVAQITQFYEAEBEYAEFPRTYLEGECLELLRRYLENGKETLQ 204
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOETODTVELVETRPAGDGT 240
DB 205 RTDAPKTHMTHAVSDHEATLRCWALGFYPAEITLTWQDGEBOETODTVELVETRPAGDGT 264
QY 241 FQKAAVVVPVSGEQRYTCHVQHEGLPQPLILRW 274
DB 265 FQKAAVVVPVSGEQRYTCHVQHEGLPQPLILRW 298

RESULT 4

US-08-652-265-23
; Sequence 23, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/652,265
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..365
; OTHER INFORMATION: /note= "Human Major Histocompatibility
; CLASS I (MHC) protein"
US-08-652-265-23

Query Match 77.1%; Score 1154; DB 3; Length 365;
Best Local Similarity 77.0%; Pred. No. 1e-104;
Matches 211; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLYFSTAVSRPGGEPRIYAVYDDTQFLRFDSDAAIPRMEPRPWPVEGPOYW 60
DB 25 GSHSMRYFSTSVSRPGGEPRIYAVYDDTQFLRFDSDAAIPRMEPRPWPVEGPOYW 84
QY 61 EMTTGYAKANAQDRVALNLLRRYNOSEAGSHTLQGMNGCDMPDGRLLRGVHQHAYDG 120
DB 85 DGETRKVKAHQTHRVLDLTLRGVYNOSEAGSHTLQGMNGCDMPDGRLLRGVHQHAYDG 144
QY 121 KDYISLNEDLSRWTAAADTVAQITQFYEAEBEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
DB 145 KDYIALKEDLSRWTAAADTVAQITQFYEAEBEYAEFPRTYLEGECLELLRRYLENGKETLQ 204
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOETODTVELVETRPAGDGT 240
DB 205 RTDAPKTHMTHAVSDHEATLRCWALGFYPAEITLTWQDGEBOETODTVELVETRPAGDGT 264
QY 241 FQKAAVVVPVSGEQRYTCHVQHEGLPQPLILRW 274
DB 265 FQKAAVVVPVSGEQRYTCHVQHEGLPQPLILRW 298

RESULT 5

US-08-834-497A-23
; Sequence 23, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/652,265
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:

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/ TELEPHONE: 650-493-4935
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 365 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..365
/ OTHER INFORMATION: /note= "Human Major Histocompatibility
/ CLASS I (MHC) protein"
US-08-834-497A-23

Query Match 77.1%; Score 1154; DB 3; Length 365;
Best Local Similarity 77.0%; Pred. No. 1e-104;
Matches 211; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGEGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQSGPYW 60
DB 25 GSHSMRYFTSVSRGEGEPRIYAVGVDDTQFVRFDSDAASQRMPEPRAPWIEQSGPEYW 84

QY 61 EWTTGYAKANQTDVALNLLRRYNSQSEAGSHTLQMGNGCDMGDPGRLLRGYHQAIDG 120
DB 85 DGETRKVAHSQTHRVLDLTLRGYNSQSEAGSHTLQMGNGCDMGDPGRLLRGYHQAIDG 144

QY 121 KDYISLNEILRSWTAADTVAQITQRFYAEAEYAEFRITYLEGECELELLRLRYLNGKETLQ 180
DB 145 KDYIALKEDLSWTAADTVAQITQRFYAEAEYAEFRITYLEGECELELLRLRYLNGKETLQ 204

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRGEBEOTQDTLVEVTRPAGDGT 240
DB 205 RTDAPKTHMTTHAVSDHEATLRCWALGFYPAEITLTWQRGEBEOTQDTLVEVTRPAGDGT 264

QY 241 FOKWAAVVVPSGEGQRYTCHVQHGSLPOPLILRW 274
DB 265 FOKWAAVVVPSGEGQRYTCHVQHGSLPOPLILRW 298

RESULT 6
US-08-370-476-100
/ Sequence 100, Application US/08370476
/ Patent No. 6153408
/ GENERAL INFORMATION:
/ APPLICANT: Mottez, Estelle
/ APPLICANT: Abastado, Jean-Pierre
/ APPLICANT: Kourilsky, Philippe
/ APPLICANT: Lene, Yu-Chun
/ APPLICANT: Ofcius, David
/ APPLICANT: Casrouge, Amanda
/ TITLE OF INVENTION: Altered Major Histocompatibility Complex
/ NUMBER OF SEQUENCES: 127
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESSEE: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/370,476
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:

TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..365
OTHER INFORMATION: /note= "Human Major Histocompatibility
CLASS I (MHC) protein"
US-08-834-497A-23

Query Match 77.1%; Score 1154; DB 3; Length 365;
Best Local Similarity 77.0%; Pred. No. 1e-104;
Matches 211; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGEGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQSGPYW 60
DB 25 GSHSMRYFTSVSRGEGEPRIYAVGVDDTQFVRFDSDAASQRMPEPRAPWIEQSGPEYW 84

QY 61 EWTTGYAKANQTDVALNLLRRYNSQSEAGSHTLQMGNGCDMGDPGRLLRGYHQAIDG 120
DB 85 DGETRKVAHSQTHRVLDLTLRGYNSQSEAGSHTLQMGNGCDMGDPGRLLRGYHQAIDG 144

QY 121 KDYISLNEILRSWTAADTVAQITQRFYAEAEYAEFRITYLEGECELELLRLRYLNGKETLQ 180
DB 145 KDYIALKEDLSWTAADTVAQITQRFYAEAEYAEFRITYLEGECELELLRLRYLNGKETLQ 204

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRGEBEOTQDTLVEVTRPAGDGT 240
DB 205 RTDAPKTHMTTHAVSDHEATLRCWALGFYPAEITLTWQRGEBEOTQDTLVEVTRPAGDGT 264

QY 241 FOKWAAVVVPSGEGQRYTCHVQHGSLPOPLILRW 274
DB 265 FOKWAAVVVPSGEGQRYTCHVQHGSLPOPLILRW 298

RESULT 7
US-09-503-444A-23
/ Sequence 23, Application US/09503444A
/ Patent No. 6228594
/ GENERAL INFORMATION:
/ APPLICANT: Thomas, Winston J.
/ APPLICANT: Drayna, Dennis T.
/ APPLICANT: Feder, John N.
/ APPLICANT: Gnirke, Andreas
/ APPLICANT: Ruddy, David
/ APPLICANT: Tsuchihashi, Zenta
/ APPLICANT: Wolff, Roger K.
/ TITLE OF INVENTION: Hereditary Hemochromatosis Gene
/ NUMBER OF SEQUENCES: 44
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..365
; OTHER INFORMATION: /note= "Human Major Histocompatibility
; OTHER INFORMATION: Class I (MHC) protein"
; US-09-503-444A-23

Query Match 77.1%; Score 1154; DB 3; Length 365;
Best Local Similarity 77.0%; Pred. No. 1e-104;
Matches 211; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGRGEPRIYAEVYDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
Db 25 GSHSMRYFFTSVSRPGRGEPRIYAVGYDDTQFVRFDSDAASQRMPEPRAPWIEQGPYW 84
Qy 61 EWTGYAKANAQTRVALRNLRRYNQSEAGSHTLQGMGCDMPGPRLLRGYHQHAYDG 120
Db 85 DGETRKVKAHSQTHRVDLGLTGLRGYNNQSEAGSHTLQGMGCDVGSDFLRGYHQYAYDG 144
Qy 121 KDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFRYLGECLELLRRYLENGKETIQ 180
Db 145 KDYIALKEDLSRWTAADNAQAQTTRKHWEAAHVAEQLRAYLGTCVWLRRLYLENGKETIQ 204
Qy 181 RADPPKAHVHPISDHEATLRCAWLGFPYPAEITLTWQRDGEQTDTELVEPRAGDGT 240
Db 205 RTDAPKTHMTHAVSDHEATLRCAWLSFYPAEITLTWQRDGEQTDTELVEPRAGDGT 264
Qy 241 FOKWAAVVVPSGGEQRYTCHVQHEGLPOPLIRW 274
Db 265 FOKWAAVVVPSGGEQRYTCHVQHEGLPKPLTLRW 298

RESULT 8
US-08-890-719-38
; Sequence 38, Application US/08890719A
; Patent No. 6075125
; GENERAL INFORMATION:
; APPLICANT: Bacon, Larry D
; APPLICANT: Hunt, Henry D
; APPLICANT: Fulton, Janet
; TITLE OF INVENTION: Production of Antisera Specific to Major
; TITLE OF INVENTION: Histocompatibility Complex Molecules in Chickens

; FILE REFERENCE: Dkt 0064.96 - Larry D. Bacon et al.
; CURRENT APPLICATION NUMBER: US/08/890,719A
; CURRENT FILING DATE: 1997-07-09
; EARLIER APPLICATION NUMBER: 60/021,665
; EARLIER FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-890-719-38

Query Match 77.1%; Score 1153; DB 3; Length 341;
Best Local Similarity 76.6%; Pred. No. 1.1e-104;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGRGEPRIYAEVYDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
Db 1 GSHSMRYFFTSVSRPGRGEPRIYAVGYDDTQFVRFDSDAASQRMPEPRAPWIEQGPYW 60
Qy 61 EWTGYAKANAQTRVALRNLRRYNQSEAGSHTLQGMGCDMPGPRLLRGYHQHAYDG 120
Db 61 DGETRKVKAHSQTHRVDLGLTGLRGYNNQSEAGSHTVQRMGCDVGSDFLRGYHQYAYDG 120
Qy 121 KDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFRYLGECLELLRRYLENGKETIQ 180
Db 121 KDYIALKEDLSRWTAADNAQAQTTRKHWEAAHVAEQLRAYLGTCVWLRRLYLENGKETIQ 180
Qy 181 RADPPKAHVHPISDHEATLRCAWLGFPYPAEITLTWQRDGEQTDTELVEPRAGDGT 240
Db 181 RTDAPKTHMTHAVSDHEATLRCAWLSFYPAEITLTWQRDGEQTDTELVEPRAGDGT 240
Qy 241 FOKWAAVVVPSGGEQRYTCHVQHEGLPOPLIRW 274
Db 241 FOKWAAVVVPSGGEQRYTCHVQHEGLPKPLTLRW 274

RESULT 9
US-08-484-905-99
; Sequence 99, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS-/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
```

```

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-99

Query Match 76.9%; Score 1151; DB 2; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 23; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRVSTAVSRPGCEPRYIAVYVDDTQFLRFSDAAIPRMPEPRPWEQEGPQYW 60
Db 25 GSHSMRYFTSVSRPGCEPRFIAGVYDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYW 84
Qy 61 EWTGYAKANAQTRVALNRLRRYNOSEAGSHTLQMGNGCDMGPDGRLLRGYHQYADG 120
Db 85 DGETRKVAHSQTHRVLDLSTLRGYNOSEAGSHTVORMYGCVDGSDGRFLRGYHQYADG 144
Qy 121 KDYISLNDLSWTAAADTVAQITQRFYEAEVEAEFRYLEGECLELLRRLYLENGKETLQ 180
Db 145 KDYLAKEDLSWTAAADMAAQTTHKWEAHVAEQWYALEGTCVZWRLRYLENGKETLQ 204
Qy 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOQDTDELVETRPAGDGT 240
Db 205 RTDAPKTHMTHAVSDHEATLRCWALSFPYAEITLTWQDGEDQDTDELVETRPAGDGT 264
Qy 241 FQKWAUVVPSGGEQRYTCHVQHEGLPQLILRW 274
Db 265 FQKWAUVVPSGGEQRYTCHVQHEGLPKPLTLPLW 298

RESULT 10
US-08-484-905-104
; Sequence 104, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS-/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 03-DEC-1991
; CLASSIFICATION: 530

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-104

Query Match 76.9%; Score 1151; DB 2; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 23; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRVSTAVSRPGCEPRYIAVYVDDTQFLRFSDAAIPRMPEPRPWEQEGPQYW 60
Db 25 GSHSMRYFTSVSRPGCEPRFIAGVYDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYW 84
Qy 61 EWTGYAKANAQTRVALNRLRRYNOSEAGSHTLQMGNGCDMGPDGRLLRGYHQYADG 120
Db 85 DGETRKVAHSQTHRVLDLSTLRGYNOSEAGSHTVORMYGCVDGSDGRFLRGYHQYADG 144
Qy 121 KDYISLNDLSWTAAADTVAQITQRFYEAEVEAEFRYLEGECLELLRRLYLENGKETLQ 180
Db 145 KDYLAKEDLSWTAAADMAAQTTHKWEAHVAEQWYALEGTCVZWRLRYLENGKETLQ 204
Qy 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOQDTDELVETRPAGDGT 240
Db 205 RTDAPKTHMTHAVSDHEATLRCWALSFPYAEITLTWQDGEDQDTDELVETRPAGDGT 264
Qy 241 FQKWAUVVPSGGEQRYTCHVQHEGLPQLILRW 274
Db 265 FQKWAUVVPSGGEQRYTCHVQHEGLPKPLTLPLW 298

RESULT 11
US-08-481-985B-99
; Sequence 99, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS-/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 03-DEC-1991
; CLASSIFICATION: 530
```

```

; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-99

Query Match 76.9%; Score 1151; DB 3; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 23; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRYIAVYVDDTQFLRFDSDAAIPRMEPRFPWVEQEGPQYW 60
DB 25 GSHSMRYFTSVSRPGRGEPRFIAGVYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYW 84
QY 61 EWTGYAKANAQTRVALRNLLRRYNQSEAGSHTLQMGNCMDGPDGRLRGYHQHAYDG 120
DB 85 DGETRKYKAHSQTHRVLDLSTLRGYNQSEAGSHTVQMTGYCDVGSDDGRFLRGYHQHAYDG 144
QY 121 KDVISLNEEDLSRTAADTVAQITQRFYEAEBEFTYLEGCELELLRLRYLENGKETLQ 180
DB 145 KDVIKEDLSRTADMAAQTKKWEAHEAQWRAYLEGTCVWLRRLRYLENGKETLQ 204
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQOTQDTLVELTRPAGDGT 240
DB 205 RTDAPKTHMTHAVSDHEATLRCWALSFPYPAEITLTWQRDGEQOTQDTLVELTRPAGDGT 264
QY 241 FOKWAAVVVPSGGEORYTCHVQHEGLPOPLILRW 274
DB 265 FOKWAAVVVPSGGEORYTCHVQHEGLPKPLTLFW 298

RESULT 12
; Sequence 104, Application US/08481985B
; Patent No. 601146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481.985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-104

Query Match 76.9%; Score 1151; DB 3; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 22; Mismatches 43; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRYIAVYVDDTQFLRFDSDAAIPRMEPRFPWVEQEGPQYW 60
DB 25 GSHSMRYFTSVSRPGRGEPRFIAGVYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYW 84
QY 61 EWTGYAKANAQTRVALRNLLRRYNQSEAGSHTLQMGNCMDGPDGRLRGYHQHAYDG 120
DB 85 DFNTENVAQSQTRVDLSTLRGYNQSEAGSHTIQMGYCDVGSDDGRFLRGYRDAYDG 144
QY 121 KDVISLNEEDLSRTAADTVAQITQRFYEAEBEFTYLEGCELELLRLRYLENGKETLQ 180
DB 145 KDVIKEDLSRTADMAAQTKKWEAHEAQWRAYLEGTCVWLRRLRYLENGKETLQ 204
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQOTQDTLVELTRPAGDGT 240
DB 205 RTDAPKTHMTHAVSDHEATLRCWALSFPYPAEITLTWQRDGEQOTQDTLVELTRPAGDGT 264
QY 241 FOKWAAVVVPSGGEORYTCHVQHEGLPOPLILRW 274
DB 265 FOKWAAVVVPSGGEORYTCHVQHEGLPKPLTLFW 298

RESULT 13
; Sequence 99, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Casrouge, Armanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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/ TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
/ TITLE OF INVENTION: Determinant
/ NUMBER OF SEQUENCES: 127
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESSEE: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS-/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,905
/ FILING DATE: 07-JUNE-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/801,818
/ FILING DATE: 05-DEC-1991
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/792,473
/ FILING DATE: 15-NOV-1991
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E. R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 03495.0106-03000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 107:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 274 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-484-905-107

Query Match : 76.9%; Score 1150; DB 2; Length 274;
Best Local Similarity 76.6%; Pred. No. 1.7e-104;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRYFTAVSRPGRGSPRYIAVYVDOTQFLRFDSDAAIPRMEPRPWPVEQSGPQYW 60
Db 1 GSHSMRYFFTSVSRPGRGSPRFTIAGVYDDTQVRFDSDAASRRMEPRAPWIEQGEPEYW 60

Qy 61 EMTTGAKANAQTDYVALRNLRLRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 120
Db 61 DGETRKVKAKSQTHRVLDLSTLRGYNQSEAGSHTLQRMTCGDVGSDFRFLRGYHQYAYDG 120

Qy 121 KQYISLNEDLRSWTAADTVAQTQRFYEAEBEYAEFRTYLEGCELELLRRYLENGKETLQ 180
Db 121 KQYIALKEDLRSWTAADMAAQTTHKWEAAHVAEQWRAYLEGTCVWLSRYLENGKETLQ 180

Qy 181 RADPPKAHVAAHPISEHATLRCWALGFYPABITLTWQDGEQOTDTLVETRPAGDGT 240
Db 181 RTDAPKTHTHAVSDHEATLRCWALGFYPABITLTWQDGEDQTDTLVETRPAGDGT 240

Qy 241 FQKWAQVVPVSGEEQRYTCHVQHEGLPQPLILRW 274
Db 241 FQKWAQVVPVSGEEQRYTCHVQHEGLPKPLTLPW 274

Search completed: June 18, 2004, 19:28:39
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:18:00 ; Search time 50 Seconds
(without alignments)
1547.079 Million cell updates/sec

Title: US-09-819-371-5
Perfect score: 1496
Sequence: 1 GSHSLRYFSTAVSRGEGEP.....QRYTCHVQHGLPQLILRW 274

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US09A_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1496	100.0	274	12	US-09-819-371-5
2	1496	100.0	362	12	US-10-257-021-82
3	1496	100.0	462	16	US-10-408-765A-1887
4	1489	99.5	362	12	US-09-819-371-4
5	1311	87.6	271	9	US-09-925-301-1431
6	1184	79.1	326	12	US-10-380-880-7
7	1174.5	78.5	379	12	US-10-210-172-160
8	1174.5	78.5	379	15	US-10-093-463-78
9	1164	77.8	215	12	US-09-819-371-6
10	1158	77.4	364	15	US-10-093-463-80
11	1154	77.1	365	14	US-10-138-888-23
12	1153	77.1	280	14	US-10-073-300-6
13	1153	77.1	280	16	US-10-075-257-6
14	1153	77.1	415	14	US-10-073-300-5
15	1153	77.1	415	16	US-10-075-257-5

ALIGNMENTS

RESULT 1

US-09-819-371-5
; Sequence 5, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-5

Query Match 100.0%; Score 1496; DB 12; Length 274;
Best Local Similarity 100.0%; Pred. No. 2.6e-140; Indels 0; Gaps 0;
Matches 274; Conservative 0; Mismatches 0;

Qy	1	GSHSLRYFSTAVSRGEGEPYIAVEYDDTQFLRFDSDAAIPRMEPREPWVEGPOYW	60
Db	1	GSHSLRYFSTAVSRGEGEPYIAVEYDDTQFLRFDSDAAIPRMEPREPWVEGPOYW	60
Qy	61	EWTGTYAKANAQTRVALNRLRYNSEAGSHYLOQNGCDMGPDGRLLEGYQHAYDG	120
Db	61	EWTGTYAKANAQTRVALNRLRYNSEAGSHYLOQNGCDMGPDGRLLEGYQHAYDG	120
Qy	121	KDYSLNEDLSWTAADTVAOITQFYAEABYAEFFRYLGECELELLRRLYLENGKETLQ	180
Db	121	KDYSLNEDLSWTAADTVAOITQFYAEABYAEFFRYLGECELELLRRLYLENGKETLQ	180
Qy	181	RADPPKAVHAHPISDHEATLRCWALGFYPABITLTWQDGESEQTQDTLVEVTRPAGDGT	240
Db	181	RADPPKAVHAHPISDHEATLRCWALGFYPABITLTWQDGESEQTQDTLVEVTRPAGDGT	240

Db 262 FQWAAVVPSEGEQRYTCHVQHEGLPQPLILRW 295
|||||
RESULT 5
US-09-925-301-1431
; Sequence 1431, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1431
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1431
Query Match 87.6%; Score 1311; DB 9; Length 271;
Best Local Similarity 99.6%; Pred. No. 6.5e-122;
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPRFVWQEGPQYW 60
DB 28 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPRFVWQEGPQYW 87
QY 61 EWTTCYAKANAQDRVALNRLRRYNQSEAGSHTLQWNGCDMGPDGRLLRGYHQAIDG 120
DB 88 EWTTCYAKANAQDRVALNRLRRYNQSEAGSHTLQWNGCDMGPDGRLLRGYHQAIDG 147
QY 121 KQYISLNEDLSRWSAATVAQITQRTYEAEBYAEFFRTYLEGECLELLRRLRYLENGKETIQ 180
DB 148 KQYISLNEDLSRWSAATVAQITQRTYEAEBYAEFFRTYLEGECLELLRRLRYLENGKETIQ 207
QY 181 RADPPKAAVHAHPISDHEATLRCWALGFYPABITLTWQDGBEOTDTTELVTREPAGDGT 240
DB 208 RADPPKAAVHAHPISDHEATLRCWALGFYPABITLTWQDGBEOTDTTELVTREPAGDGT 267
QY 241 FQ 242
DB 268 FR 269
RESULT 6
US-10-380-880-7
; Sequence 7, Application US/10380880
; Publication No. US20040044182A1
; GENERAL INFORMATION:
; APPLICANT: Hunt, Joan S.
; APPLICANT: Morales, Pedro J.
; APPLICANT: Petroff, Margaret G.
; TITLE OF INVENTION: EXPRESSION, PREPARATION, USES, AND SEQUENCE OF RECOMBINANTLY-DERIVED
; FILE REFERENCE: SOLUBLE HLA-G
; CURRENT APPLICATION NUMBER: US/10/380,880
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/232,761
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-880-7

Query Match 79.1%; Score 1184; DB 12; Length 326;
Best Local Similarity 78.8%; Pred. No. 3.7e-109;
Matches 216; Conservative 22; Mismatches 36; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPRFVWQEGPQYW 60
DB 32 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPRFVWQEGPQYW 91
QY 61 EWTTCYAKANAQDRVALNRLRRYNQSEAGSHTLQWNGCDMGPDGRLLRGYHQAIDG 120
DB 92 EWTTCYAKANAQDRVALNRLRRYNQSEAGSHTLQWNGCDMGPDGRLLRGYHQAIDG 151
QY 121 KQYISLNEDLSRWSAATVAQITQRTYEAEBYAEFFRTYLEGECLELLRRLRYLENGKETIQ 180
DB 152 KQYISLNEDLSRWSAATVAQITQRTYEAEBYAEFFRTYLEGECLELLRRLRYLENGKETIQ 211
QY 181 RADPPKAAVHAHPISDHEATLRCWALGFYPABITLTWQDGBEOTDTTELVTREPAGDGT 240
DB 212 RADPPKAAVHAHPISDHEATLRCWALGFYPABITLTWQDGBEOTDTTELVTREPAGDGT 271
QY 241 FQWAAVVPSEGEQRYTCHVQHEGLPQPLILRW 274
DB 272 FQWAAVVPSEGEQRYTCHVQHEGLPQPLILRW 305
RESULT 7
US-10-210-172-160
; Sequence 160, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shinkets, Richard
; APPLICANT: Zertusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalte, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03


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; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 160
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-160

Query Match      78.5%; Score 1174.5; DB 12; Length 379;
Best Local Similarity 78.0%; Pred. No. 4e-108;
Matches 216; Conservative 22; Mismatches 36; Indels 3; Gaps 1;

QY 1 GSHSLRYFSTAVSRPGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPYW 60
DB 25 GSHSNRYFSAVSRPGGEPRFIAMGYVDDTQFVRFDSDSACPRMEPRAPWVEQGPYW 84
QY 61 EWTGYAKANAQTRVALNRLNRYNQA---GSHTLQMGNGCDMGDPGRLLRGVHOA 117
DB 85 EETRNTKAHAQTRDMNLQTLRGYNQSGVPGSGHTLQMGNGCDLGSGRLLRGVEYA 144
QY 118 YDGKDYISLNEDLSRSTAADTVAQITQFYBAEYAEFFRTRYLGECELELRLRYLENGKE 177
DB 145 YDGKDYIALNEDLSRSTAADTAAQISKRKCEANVAQRRAYLEGTCTVEWLHRYLENGKE 204
QY 178 TLQRADPPKAVHAHPISDHEATRLCVALGYPAEIITLTWDRGEEQOTDTVELVETPAG 237
DB 205 MLQRADPPKTVTHHPVDYEAATRLCVALGYPAEIITLTWDRGEEQOTDTVELVETPAG 264
QY 238 DGTQKAAVVPVSGEORYTCHVQHEGLPOPLRLW 274
DB 265 DGTQKAAVVPVSGEORYTCHVQHEGLPFLMLRW 301

RESULT 8
US-10-093-463-78
; Sequence 78, Application US/10093463
; Publication No. US20030208039A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir
; APPLICANT: Pochart, Pascal
; APPLICANT: Zhong, Mei
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glenda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zethusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Pena, Carol
; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly
```

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; APPLICANT: Gorman, Linda
; APPLICANT: Spaderna, Steven
; APPLICANT: Voss, Edward
; APPLICANT: Malyankar, Uriel
; APPLICANT: Anderson, David
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; TITLE OF INVENTION: No. US20030208039A1el Antibodies that Bind to Antigenic Polypep
; FILE OF INVENTION: Encoding The Antigens, and Methods of Use.
; FILE REFERENCE: 21402-290A (Cura 590AT)
; CURRENT APPLICATION NUMBER: US/10/093,463
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/283,675
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,101
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-093-463-78

Query Match      78.5%; Score 1174.5; DB 15; Length 379;
Best Local Similarity 78.0%; Pred. No. 4e-108;
Matches 216; Conservative 22; Mismatches 36; Indels 3; Gaps 1;

QY 1 GSHSLRYFSTAVSRPGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPYW 60
DB 25 GSHSNRYFSAVSRPGGEPRFIAMGYVDDTQFVRFDSDSACPRMEPRAPWVEQGPYW 84
QY 61 EWTGYAKANAQTRVALNRLNRYNQA---GSHTLQMGNGCDMGDPGRLLRGVHOA 117
DB 85 EETRNTKAHAQTRDMNLQTLRGYNQSGVPGSGHTLQMGNGCDLGSGRLLRGVEYA 144
QY 118 YDGKDYISLNEDLSRSTAADTVAQITQFYBAEYAEFFRTRYLGECELELRLRYLENGKE 177
DB 145 YDGKDYIALNEDLSRSTAADTAAQISKRKCEANVAQRRAYLEGTCTVEWLHRYLENGKE 204
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QY 178 TLORADPPKAAVHHPISDHEATLRCWALGFYPABITLITWDRGEOTQDTLVELTRPAG 237
DB 205 MLQADPPKTHVTHHVFVFEATLRCWALGFYPABITLITWDRGEDQDTLVELTRPAG 264
QY 238 DGTFFQKAAVVPVSGEGEQRXYTHVQHEGLPQPLILRW 274
DB 265 DGTFFQKAAVVPVSGEGEQRXYTHVQHEGLPEPLILRW 301

RESULT 9

US-09-819-371-6
; Sequence 6, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-6

Query Match 77.8%; Score 1164; DB 12; Length 215;
Best Local Similarity 99.5%; Pred. No. 2e-107;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQSGPQVWETTCYAKANAQTDRAVLRNLL 82
DB 1 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQSGPQVWETTCYAKANAQTDRAVLRNLL 60
QY 83 RRYNQSEAGSHTLQGMNGCDMGDPGRLLRGYHAYDGDYIYSLNEDLSRWTAAADTVAQI 142
DB 61 RRYNQSEAGSHTLQGMNGCDMGDPGRLLRGYHAYDGDYIYSLNEDLSRWTAAADTVAQI 120
QY 143 TQFYAEAEVABFRITVLEGECLLRRLRYLNGKETLQRADPPKAAVHHPISDHEATLR 202
DB 121 TQFYAEAEVABFRITVLEGECLLRRLRYLNGKETLQRADPPKAAVHHPISDHEATLR 180
QY 203 CWALGFYPABITLITWDRGEOTQDTLVELTRPAG 237
DB 181 CWALGFYPABITLITWDRGEOTQDTLVELTRPAG 215

RESULT 10

US-10-093-463-80
; Sequence 80, Application US/10093463
; Publication No. US20030208039A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir
; APPLICANT: Pochart, Pascal
; APPLICANT: Zhong, Mei
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glenda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerkusen, Bryan
; APPLICANT: Tcherenev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Pena, Carol

; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gorman, Linda
; APPLICANT: Spaderna, Steven
; APPLICANT: Voss, Edward
; APPLICANT: Malyankar, Uriel
; APPLICANT: Anderson, David
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; TITLE OF INVENTION: No. US20030208039A1 Antibodies that Bind to Antigenic Polypept
; FILE REFERENCE: 21402-290A (Cura 590AT)
; CURRENT APPLICATION NUMBER: US/10/093,463
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/283,675
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,101
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-093-463-80

Query Match 77.4%; Score 1158; DB 15; Length 364;

Best Local Similarity 77.4%; Pred. No. 1.7e-106;
Matches 212; Conservative 25; Mismatches 37; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGEGEPRIYAVYVDQTLRFDSDAAIPRMEPREPWVEQSGPQVW 60

DB 25 GSHSLRYFSTAVSRGEGEPRIYAVYVDQTLRFDSDAAIPRMEPREPWVEQSGLEW 84

QY 61 EWTGYSKANAQTDRAVLRNLLRYNQSEAGSHITQGMNGCDMGDPGRLLRGYHAYDGD 120

DB 85 DQETRNAKHAQIYRVNLTLLRYNQSEAGSHITQGMNGCDMGDPGRLLRGYHAYDGD 144

QY 121 KDYISLNEQLRSWTAAADTVAQITQFYAEAEVABFRITVLEGECLLRRLRYLNGKETLQ 180

Db 145 KDYLALNEDLSHTAANTAAQISQKWEADRYSEQVAYLEGGKMEWRRLHLENGKETLQ 204
Qy 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTQDTLVELTRPAGDGT 240
Db 205 HADPPKAHVTHQPSIDHEATLRCWALGLYPAEITLTWQDGEDQDTQDTLVELTRPAGDGT 264
Qy 241 FQKWAAVVPSGEGEORYTCHVOHEGLPQPLILRW 274
Db 265 FQKWAAVVPSGEGEORYTCHVOHEGLPEPLTLRW 298

RESULT 11

US-10-138-888-23
; Sequence 23, Application US/1013888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Teuchihasi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..365
OTHER INFORMATION: /note= "Human Major Histocompatibility Class I (MHC) protein"

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-138-888-23

Query Match 77.1%; Score 1154; DB 14; Length 365;
Best Local Similarity 77.0%; Pred. No. 4.1e-106;
Matches 211; Conservative 21; Mismatches 42; Indels 0; Gaps 0;
Qy 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPRPWPVEQEGPQYW 60
Db 25 GSHSMRYFTTSVSRPGRGEPRIYAVYVDDTQFLRFDSDAAISQRMFPRAPWIEQEGPEYW 84
Qy 61 EWTGTGAKANAQTDRLVALNRLRRYNSQSEAGSHTLQMGNGCDMGDPDGRLLRGYHQHAYDG 120
Db 85 DGETRKYKAHSQTHRVLDGLTGLRGYTNQSEAGSHTLQMGFGCDVGSDFRFLRGYHQHAYDG 144
Qy 121 KDYISLNEDLSRWTAAQITQRFYAEYAEYAEPRTYLEGECELELLRRLRYLENGKETLQ 180
Db 145 KDYIALKEDLSRWTAAQITQTKKWEAAHVAEQRLAVLEGTCTVEWLRRLRYLENGKETLQ 204
Qy 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTQDTLVELTRPAGDGT 240
Db 205 RTDAPKTHMTHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQDTQDTLVELTRPAGDGT 264
Qy 241 FQKWAAVVPSGEGEORYTCHVOHEGLPQPLILRW 274
Db 265 FQKWAAVVPSGEGEORYTCHVOHEGLPKPLTLRW 298

RESULT 12

US-10-073-300-6
; Sequence 6, Application US/10073300
; Publication No. US20030003535A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,300
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-073-300-6

Query Match 77.1%; Score 1153; DB 14; Length 280;
Best Local Similarity 76.6%; Pred. No. 3.6e-106;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPRPWPVEQEGPQYW 60
Db 1 GSHSMRYFTTSVSRPGRGEPRIYAVYVDDTQFLRFDSDAAISQRMFPRAPWIEQEGPEYW 60
Qy 61 EWTGTGAKANAQTDRLVALNRLRRYNSQSEAGSHTLQMGNGCDMGDPDGRLLRGYHQHAYDG 120
Db 61 DGETRKYKAHSQTHRVLDGLTGLRGYTNQSEAGSHTLQMGFGCDVGSDFRFLRGYHQHAYDG 120
Qy 121 KDYISLNEDLSRWTAAQITQRFYAEYAEYAEPRTYLEGECELELLRRLRYLENGKETLQ 180
Db 121 KDYIALKEDLSRWTAAQITQTKKWEAAHVAEQRLAVLEGTCTVEWLRRLRYLENGKETLQ 180
Qy 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTQDTLVELTRPAGDGT 240
Db 181 RTDAPKTHMTHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQDTQDTLVELTRPAGDGT 240
Qy 241 FQKWAAVVPSGEGEORYTCHVOHEGLPQPLILRW 274
Db 241 FQKWAAVVPSGEGEORYTCHVOHEGLPKPLTLRW 274

RESULT 13

US-10-075-257-6
; Sequence 6, Application US/10075257
; Publication No. US20040086960A1
; GENERAL INFORMATION:

```
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
; FILE REFERENCE: 02/23338
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-075-257-6

Query Match
Best Local Similarity 77.1%; Score 1153; DB 16; Length 280;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGPRYIAVEYVDDTQFLRPSDAAIPRMEPRPVEQGPQYW 60
DB 1 GSHSMRYFTSVSRPGEGPRFIAGVYVDDTQFVRPDSDAASQRMPEPRAPWIEQGPY 175
QY 61 EWTTCYAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNGCDMGPDGRLRLRGYHQA 120
DB 61 DGETRKVKVHSAQTHRVLDLGLRGYNSQAGSHTVQRMVYCDVGSDFRFLRGYHQA 120
QY 121 KOYISLNEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180
DB 121 KOYIALKEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180
QY 181 RADPPKAVHAPHSIDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAGDGT 240
DB 181 RTDAPKTHMTHAVSDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAGDGT 240
QY 241 FQKWAAVVVPVSGEQRITVCHVQHEGLPKPLTLRW 274
DB 241 FQKWAAVVVPVSGEQRITVCHVQHEGLPKPLTLRW 274

RESULT 14
US-10-073-300-5
; Sequence 5, Application US/10073300
; Publication No. US20030003535A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,300
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human beta2 microglobulin linked to MHC class I heavy chain
US-10-073-300-5

Query Match
Best Local Similarity 77.1%; Score 1153; DB 14; Length 415;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGPRYIAVEYVDDTQFLRPSDAAIPRMEPRPVEQGPQYW 60
DB 116 GSHSMRYFTSVSRPGEGPRFIAGVYVDDTQFVRPDSDAASQRMPEPRAPWIEQGPY 175
QY 61 EWTTCYAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNGCDMGPDGRLRLRGYHQA 120
DB 176 DGETRKVKVHSAQTHRVLDLGLRGYNSQAGSHTVQRMVYCDVGSDFRFLRGYHQA 235
QY 121 KOYISLNEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180
DB 121 KOYIALKEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180

RESULT 15
US-10-075-257-5
; Sequence 5, Application US/10075257
; Publication No. US20040086960A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
; FILE REFERENCE: 02/23338
; CURRENT APPLICATION NUMBER: US/10/075,257
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human beta2 microglobulin linked to MHC class I heavy chain
US-10-075-257-5

Query Match
Best Local Similarity 77.1%; Score 1153; DB 16; Length 415;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGPRYIAVEYVDDTQFLRPSDAAIPRMEPRPVEQGPQYW 60
DB 116 GSHSMRYFTSVSRPGEGPRFIAGVYVDDTQFVRPDSDAASQRMPEPRAPWIEQGPY 175
QY 61 EWTTCYAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNGCDMGPDGRLRLRGYHQA 120
DB 176 DGETRKVKVHSAQTHRVLDLGLRGYNSQAGSHTVQRMVYCDVGSDFRFLRGYHQA 235
QY 121 KOYISLNEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180
DB 236 KOYIALKEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 295
QY 181 RADPPKAVHAPHSIDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAGDGT 240
DB 296 RTDAPKTHMTHAVSDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAGDGT 355
QY 241 FQKWAAVVVPVSGEQRITVCHVQHEGLPKPLTLRW 274
DB 356 FQKWAAVVVPVSGEQRITVCHVQHEGLPKPLTLRW 389

Search completed: June 18, 2004, 19:22:13
Job time : 52 secs
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; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
; FILE REFERENCE: 02/23338
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-075-257-6

Query Match
Best Local Similarity 77.1%; Score 1153; DB 16; Length 280;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGPRYIAVEYVDDTQFLRPSDAAIPRMEPRPVEQGPQYW 60
DB 1 GSHSMRYFTSVSRPGEGPRFIAGVYVDDTQFVRPDSDAASQRMPEPRAPWIEQGPY 175
QY 61 EWTTCYAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNGCDMGPDGRLRLRGYHQA 120
DB 61 DGETRKVKVHSAQTHRVLDLGLRGYNSQAGSHTVQRMVYCDVGSDFRFLRGYHQA 120
QY 121 KOYISLNEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180
DB 121 KOYIALKEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180
QY 181 RADPPKAVHAPHSIDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAGDGT 240
DB 181 RTDAPKTHMTHAVSDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAGDGT 240
QY 241 FQKWAAVVVPVSGEQRITVCHVQHEGLPKPLTLRW 274
DB 241 FQKWAAVVVPVSGEQRITVCHVQHEGLPKPLTLRW 274

RESULT 14
US-10-073-300-5
; Sequence 5, Application US/10073300
; Publication No. US20030003535A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,300
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human beta2 microglobulin linked to MHC class I heavy chain
US-10-073-300-5

Query Match
Best Local Similarity 77.1%; Score 1153; DB 14; Length 415;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGPRYIAVEYVDDTQFLRPSDAAIPRMEPRPVEQGPQYW 60
DB 116 GSHSMRYFTSVSRPGEGPRFIAGVYVDDTQFVRPDSDAASQRMPEPRAPWIEQGPY 175
QY 61 EWTTCYAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNGCDMGPDGRLRLRGYHQA 120
DB 176 DGETRKVKVHSAQTHRVLDLGLRGYNSQAGSHTVQRMVYCDVGSDFRFLRGYHQA 235
QY 121 KOYISLNEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180
DB 121 KOYIALKEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180

RESULT 15
US-10-075-257-5
; Sequence 5, Application US/10075257
; Publication No. US20040086960A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
; FILE REFERENCE: 02/23338
; CURRENT APPLICATION NUMBER: US/10/075,257
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human beta2 microglobulin linked to MHC class I heavy chain
US-10-075-257-5

Query Match
Best Local Similarity 77.1%; Score 1153; DB 16; Length 415;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGPRYIAVEYVDDTQFLRPSDAAIPRMEPRPVEQGPQYW 60
DB 116 GSHSMRYFTSVSRPGEGPRFIAGVYVDDTQFVRPDSDAASQRMPEPRAPWIEQGPY 175
QY 61 EWTTCYAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNGCDMGPDGRLRLRGYHQA 120
DB 176 DGETRKVKVHSAQTHRVLDLGLRGYNSQAGSHTVQRMVYCDVGSDFRFLRGYHQA 235
QY 121 KOYISLNEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 180
DB 236 KOYIALKEDLRSAADTAADTAQITQRFYAEYAEAEFFRYLGECELELLRRYLENGKET 295
QY 181 RADPPKAVHAPHSIDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAGDGT 240
DB 296 RTDAPKTHMTHAVSDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVEVTRPAGDGT 355
QY 241 FQKWAAVVVPVSGEQRITVCHVQHEGLPKPLTLRW 274
DB 356 FQKWAAVVVPVSGEQRITVCHVQHEGLPKPLTLRW 389

Search completed: June 18, 2004, 19:22:13
Job time : 52 secs
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:19:06 ; Search time 18 Seconds
(without alignments)
792.623 Million cell updates/sec

Title: US-09-819-371-5
Perfect score: 1496
Sequence: 1 GSHSLRYFTAVSRPGRGP.....QRYTCHVQHEGLPQLILRW 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1496	100.0	362	1	HLAF_HUMAN
2	1471	98.3	346	1	LC28_PANTR
3	1416	94.7	348	1	HLAF_MACMU
4	1240	82.9	362	1	1B27_HUMAN
5	1228	82.1	362	1	1B03_GORGO
6	1227	82.0	362	1	1B39_HUMAN
7	1227	82.0	362	1	1B67_HUMAN
8	1226	82.0	363	1	1B73_HUMAN
9	1224	81.8	362	1	1B08_HUMAN
10	1224	81.8	362	1	1B42_HUMAN
11	1223	81.8	362	1	1B01_GORGO
12	1223	81.8	362	1	1B47_HUMAN
13	1223	81.8	365	1	1A23_HUMAN
14	1222	81.7	362	1	1B37_HUMAN
15	1221	81.6	362	1	1B02_GORGO
16	1221	81.6	362	1	1B07_HUMAN
17	1221	81.6	362	1	1B14_HUMAN
18	1221	81.6	362	1	1B46_HUMAN
19	1221	81.6	366	1	1C12_HUMAN
20	1220	81.6	362	1	1B40_HUMAN
21	1219	81.5	366	1	1C08_HUMAN
22	1218	81.4	359	1	1B01_PANTR
23	1218	81.4	362	1	1B54_HUMAN
24	1217	81.4	362	1	1B55_HUMAN
25	1216	81.3	362	1	1B56_HUMAN
26	1216	81.3	362	1	1B81_HUMAN
27	1216	81.3	365	1	1A24_HUMAN
28	1216	81.3	366	1	1C14_HUMAN
29	1215	81.2	362	1	1B02_PANTR
30	1214	81.1	362	1	1B38_HUMAN
31	1213	81.1	362	1	1B15_HUMAN
32	1212	81.0	362	1	1A02_PANTR
33	1212	81.0	362	1	1B78_HUMAN

RESULT 1

HLAF_HUMAN

ID	HLAF_HUMAN	STANDARD	PRT	362 AA
AC	P30511			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (leukocyte antigen F) (CDAL2).			
GN	HLA-F OR HLAF OR HLA-5.4.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90111605; PubMed=1688605;			
RA	Geraghty D.E., Wei X., Orr H.T., Koller B.H.;			
RT	"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive element.";			
RT	J. Exp. Med. 171:1-18(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91197889; PubMed=1707659;			
RA	Lary D., Epstein H., Holmes N.;			
RT	"The human class I MHC gene HLA-F is expressed in lymphocytes.";			
RL	Int. Immunol. 2:531-537(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Shiina S., Tamiya G., Oka A., Inoko H.;			
RT	"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.			
CC	-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; X17093; CAA34947.1; ..			
DR	EMBL; AF000521; BAB63337.1; ..			
DR	PIR; A60384; A60384.			
DR	HSSP; Q30201; 1A62.			
DR	Genew; HGNC:4963; HLA-F.			
DR	MIM; 143110; ..			
DR	GO; GO:0030106; F:MHC class I receptor activity; TAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_c1.			
DR	InterPro; IPR003006; Ig_MHC.			

34	1210	80.9	365	1	1A01_SAGOE	P30515	saguinus oe
35	1209	80.8	366	1	1C02_GORGO	P30385	gorilla gor
36	1209	80.8	366	1	1C04_GORGO	P30387	gorilla gor
37	1208	80.7	362	1	1B82_HUMAN	Q29718	homo sapien
38	1207	80.7	362	1	1B48_HUMAN	P30486	homo sapien
39	1206	80.6	366	1	1C03_GORGO	P30386	gorilla gor
40	1206	80.6	366	1	1C03_HUMAN	P04222	homo sapien
41	1205	80.5	365	1	1A30_HUMAN	P16188	homo sapien
42	1205	80.5	366	1	1C06_HUMAN	Q29963	homo sapien
43	1203	80.4	362	1	1B35_HUMAN	P30685	homo sapien
44	1203	80.4	362	1	1B59_HUMAN	Q29940	homo sapien
45	1202	80.3	362	1	1B18_HUMAN	P30466	homo sapien

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DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGCL; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 362
FT DOMAIN 22 111
FT DOMAIN 112 203
FT DOMAIN 204 295
FT DOMAIN 296 305
FT TRANSMEM 306 329
FT DOMAIN 330 362
FT DISULFID 122 185
FT DISULFID 224 280
FT CARBOHYD 107 107
SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Query Match 100.0%; Score 1496; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 4e-113;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGCEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 60
DB 22 GSHSLRYFSTAVSRPGCEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 81
QY 61 EWTGYAKANAQTDVALNLLRRYNSQSEAGSHTLQGNMGCDMPDGLRLRGYHAYDG 120
DB 82 EWTGYAKANAQTDVALNLLRRYNSQSEAGSHTLQGNMGCDMPDGLRLRGYHAYDG 141
QY 121 KDYSISNEDLRSWTAADTVAQITQRFYAEABEYAEFRYLEGECLLELLRRYLENGKETLQ 180
DB 142 KDYSISNEDLRSWTAADTVAQITQRFYAEABEYAEFRYLEGECLLELLRRYLENGKETLQ 201
QY 181 RADPPKAHVAHPISDHEATRLCWALGFYPAEITLTWQDGEQTDQTELVEPRPADGT 240
DB 202 RADPPKAHVAHPISDHEATRLCWALGFYPAEITLTWQDGEQTDQTELVEPRPADGT 261
QY 241 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
DB 262 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

RESULT 3
HLAF MACMU STANDARD; PRT; 348 AA.
ID HLAF MACMU
AC P33617;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F
DE antigen) (leukocyte antigen F).
GN HLA-F OR HLA-F.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93246295; PubMed=8482576;
RA Otting N., Bontrop R.E.;
RT "Characterization of the rhesus macaque (Macaca mulatta) equivalent
RT of HLA-F";
RL Immunogenetics 38:141-145(1993).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; Z21819; CAA79885.1; -.
DR PIR; S29990; S29990.
DR HSSP; Q30201; LA6Z.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC I; 1.
DR SMART; SM00407; Igc1-1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 348
FT -----
FT ALPHA CHAIN F.
FT DOMAIN 22 113
FT DOMAIN 114 205
FT DOMAIN 206 297
FT DOMAIN 298 307
FT TRANSMEM 308 331
FT DOMAIN 332 348
FT DISULFID 124 187
FT DISULFID 226 282
FT CARBOHYD 109 109
SQ SEQUENCE 348 AA; 39300 MW; 77BD7E9B9B1E0F7 CRC64;
Query Match 94.7%; Score 1416; DB 1; Length 348;
Best Local Similarity 94.9%; Pred. No. 1e-106;
Matches 262; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
QY 1 GSHSLRYFSTAVSRPRGEP- RYIAVEYDDTQFLRFDSDAAIPMEPRAPWVEQGPQ 58
DB 22 GSHSLRYFSTAVSRPRGEPQRYIAVSYYDDTQFLRFDSDAAIPMEPRAPWVEQGPQ 81
QY 59 YWMTTGYAKANACTRVALNRLRRYNQSEASHTLQGMNGCDMGPDGRLRLGYHQHAY 118
DB 82 YWMTTGYAKANACTRVALNRLRRYNQSEASHTLQGMNGCDMGPDGRLRLGYHQHAY 141
QY 119 DGKDYISLNDLSWTAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRLYLENGKET 178
DB 142 DGKDYISLNDLSWTAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRLYLENGKET 201

QY 179 LQRADPPKAAVHAHPISDHEATLRCWALGFPAEITLTWQDGEBOQTDTLVETREAGD 238
DB 202 LQRADPPKAAVHAHPISDHEATLRCWALGFPAEITLTWQDGEBOQTDTLVETREAGD 261
QY 239 GTFQKAAVAVVPSGEQRYTCHVQHEGLPQPLILRW 274
DB 262 GTFQKAAVAVVPSGEQRYTCHVQHEGLPQPLILRW 297
RESULT 4
ID 1B27 HUMAN STANDARD; PRT; 362 AA.
AC P03989; P10317; P10318; P19373; P30467; Q08136; Q29693; Q29846;
AC Q29861;
DT 23-OCT-1986 (Rel. 02, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-27 alpha chain precursor
DE (MHC class I antigen B*27).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*2701).
RX MEDLINE=86138405; PubMed=3912316;
RA Weiss E.H., Kuon W., Doerner C., Lang M., Riethmuller G.;
RT "Organization, sequence and expression of the HLA-B27 gene: a
RT molecular approach to analyze HLA and disease associations";
RL Immunobiology 170:367-380(1985).
RN [2]
RP SEQUENCE OF 25-361 FROM N.A. (B*2701).
RX MEDLINE=86149317; PubMed=3485286;
RA Szoets H., Riethmuller G., Weiss E., Vao T.;
RT "Complete sequence of HLA-B27 cDNA identified through the
RT characterization of structural markers unique to the HLA-A, -B, and
RT -C allelic series";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
RN [3]
RP SEQUENCE OF 25-295 (B*2701).
RX MEDLINE=85226361; PubMed=2408663;
RA Ezquerria A., Bragado R., Vega M.A., Strominger J.L., Woody J.,
RA Lopez de Castro J.A.;
RT "Primary structure of papain-solubilized human histocompatibility
RT antigen HLA-B27";
RL Biochemistry 24:1733-1741(1985).
RN [4]
RP SEQUENCE FROM N.A. (B*2701 AND B*2702).
RX MEDLINE=86220133; PubMed=3011411;
RA Seemann G.H.A., Rein R.S., Brown C.S., Ploegh H.L.;
RT "Gene conversion-like mechanisms may generate polymorphism in human
RT class I genes";
RL EMBO J. 5:547-552(1986).
RN [5]
RP SEQUENCE FROM N.A. (B*2702).
RX MEDLINE=96086486; PubMed=7482496;
RA Moses J.H., Marsh S.G.E., Arnett K.L., Adams E.J., Bodmer J.G.,
RA Parham P.;
RT "On the nucleotide sequences of B*2702 and B*2705";
RL Tissue Antigens 46:50-53(1995).
RN [6]
RP SEQUENCE OF 86-107 AND 171-181 (B*2702).
RX MEDLINE=86042671; PubMed=2414775;
RA Vega M.A., Ezquerria A., Rojo S., Aparicio P., Bragado R.,
RA Lopez de Castro J.A.;
RT "Structural analysis of an HLA-B27 functional variant: identification
RT of residues that contribute to the specificity of recognition by
RT cytolytic T lymphocytes";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
RN [7]
RP SEQUENCE FROM N.A. (B*2703).
RX MEDLINE=88227491; PubMed=3286582;

RA Choo S.Y., St John T., Orr H.T., Hansen J.A.;
 RT "Molecular analysis of the variant alloantigen HLA-B*2703 (HLA-B*2703)
 RT identifies a unique single amino acid substitution."
 RL Hum. Immunol. 21:209-219(1988).
 RN [8]
 RP SEQUENCE FROM N.A. (B*2704 AND B*2706).
 RX MEDLINE=96134006; PubMed=8550101.
 RA Rudwaleit M., Bowness P., Wordsworth P.;
 RT "The nucleotide sequence of HLA-B*2704 reveals a new amino acid
 RT substitution in exon 4 which is also present in HLA-B*2706."
 RL Immunogenetics 43:160-162(1996).
 RN [9]
 RP SEQUENCE FROM N.A. (B*2706).
 RX MEDLINE=94102824; PubMed=8276469;
 RA Vilches C., de Pablo R., Kreisler M.;
 RT "Nucleotide sequence of HLA-B*2706."
 RL Immunogenetics 39:219-219(1994).
 RN [10]
 RP SEQUENCE FROM N.A. (B*2707).
 RX MEDLINE=91268545; PubMed=1711072;
 RA Choo Y.S., Fan L.A., Hansen J.A.;
 RT "A novel HLA-B*27 allele maps B27 allospecificity to the region around
 RT position 70 in the alpha 1 domain."
 RL J. Immunol. 147:174-180(1991).
 RN [11]
 RP SEQUENCE FROM N.A. (B*2708).
 RX MEDLINE=95064789; PubMed=7974468;
 RA Hildebrand W.H., Domene J.D., Shen S.Y., Marsh S.G.E., Bunce M.,
 RA Guttridge M.G., Darke C., Parham P.;
 RT "The HLA-B*7001 antigen is encoded by a new subtype of HLA-B*27
 RT (B*2708)."
 RL Tissue Antigens 44:47-51(1994).
 RN [12]
 RP SEQUENCE FROM N.A. (B*2709).
 RX MEDLINE=94375872; PubMed=8089488;
 RA Del Porto P., D'Amato M., Florillo M.T., Tuosto L., Piccolella E.,
 RA Sorrentino R.;
 RT "Identification of a novel HLA-B*27 subtype by restriction analysis of
 RT a cytotoxic gamma/delta T cell clone."
 RL J. Immunol. 153:3093-3100(1994).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
 RX MEDLINE=92405152; PubMed=1525820;
 RA Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;
 RT "The three-dimensional structure of HLA-B*27 at 2.1-A resolution
 RT suggests a general mechanism for tight peptide binding to MHC."
 RL Cell 70:1035-1048(1992).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=92018187; PubMed=1922337;
 RA Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;
 RT "The structure of HLA-B*27 reveals nonamer self-peptides bound in an
 RT extended conformation."
 RL Nature 353:321-325(1991).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
 RX MEDLINE=22344622; PubMed=12244049;
 RA Hulsemeyer M., Hillig R.C., Voiz A., Ruhl M., Schroder W., Saenger W.,
 RA Ziegler A., Uchanska-Ziegler B.;
 RT "HLA-B*27 subtypes differentially associated with disease exhibit
 RT subtle structural alterations."
 RL J. Biol. Chem. 277:47844-47853(2002).
 RN [16]
 RP 3D-STRUCTURE MODELING OF 115-206.
 RX MEDLINE=95148615; PubMed=7846047;
 RA Rognan D., Scapozza L., Folkers G., Daser A.;
 RT "Rational design of nonnatural peptides as high-affinity ligands for
 RT the HLA-B*2705 human leukocyte antigen."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:753-757(1995).
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-

CC microglobulin).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- POLYMORPHISM: The following alleles of B-27 are known:
 CC B*2701-B*2705, B*2702 (B27.2; B-27K; B27e), B*2703 (B27d), B*2704,
 CC B*2706, B*2707, B*2708 (B7Qui) and B*2709 (B27-ci). The sequence
 CC shown is that of B*2701.
 CC -!- DISBASE: HLA-B27 is associated with the development of ankylosing
 CC spondylitis.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X03945; CAA27578.1; ALT_SEQ.
 CC EMBL; X03664; CAA27301.1; -
 CC EMBL; X03667; CAA27301.1; JOINED.
 CC EMBL; L38504; AAG69724.1; -
 CC EMBL; M54883; AAG59616.1; -
 CC EMBL; X03685; CAA27302.1; -
 CC EMBL; X03686; CAA27302.1; JOINED.
 CC EMBL; M12967; AAG36221.1; -
 CC EMBL; U27608; AAC50444.1; -
 CC EMBL; U35734; AAC50447.1; -
 CC EMBL; X73578; CAA51980.1; -
 CC EMBL; M62852; AAG59647.1; -
 CC EMBL; L19923; AAG59658.1; -
 CC EMBL; Z33453; CAA83876.1; -
 CC PIR; I37515; I37515.
 CC PIR; I56116; I56116.
 CC PIR; S07441; HLUH2.
 CC PDB; 1HSA; 15-OCT-92.
 CC PDB; 1ROG; 30-SEP-94.
 CC PDB; 1ROH; 30-SEP-94.
 CC PDB; 1ROI; 30-SEP-94.
 CC PDB; 1ROJ; 30-SEP-94.
 CC PDB; 1ROK; 30-SEP-94.
 CC PDB; 1ROL; 30-SEP-94.
 CC PDB; 1JGE; 23-DEC-02.
 CC Genew; HGNC:4932; HLA-B.
 CC MIM; 142830.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig_C1.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR001039; MHC_I.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00129; MHC_I; 1.
 CC PRINTS; PR01638; MHCCLASSI.
 CC ProDom; PD000050; MHC_I; 1.
 CC SMART; SMC0407; IgC1; 1.
 CC PROSITE; PS00835; IG_LIKE; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism;
 CC 3D-structure. 1 24
 CC SIGNAL 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 CC CHAIN B-27 ALPHA CHAIN.
 CC DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 CC DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 CC DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 CC DOMAIN 299 308 CONNECTING PEPTIDE.
 CC TRANSMEM 309 332
 CC
 CC Query Match 82.9%; Score 1240; DB 1; Length 362;
 CC Best Local Similarity 82.8%; Pred. No. 1.5e-92;
 CC Matches 227; Conservative 14; Mismatches 33; Indels 0; Gaps 0;
 CC
 CC 1 GSHSLVSTAVSRPGRGPRVIAVVDVDTQFLRFDSDAATPRMEPRPWPVEQGPQYW 60
 CC 25 GSHSMRYFTTSVSRPGRGPRFITVGVVDVDTLFRFDSDAASPRFPAPWIEQGPQYW 84


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FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 293 BY SIMILARITY.
FT VARIANT 33 33 Y--> D (in allele B*3912).
FT VARIANT 35 35 /FTID=VAR_016659.
FT VARIANT 35 35 S--> A (in allele B*3904 and allele
FT B*3912).
FT /FTID=VAR_016421.

Query Match 82.0%; Score 1227; DB 1; Length 362;
Best Local Similarity 81.8%; Pred. No. 1.7e-91;
Matches 224; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 GSHSLRYFVAVSRGPGPRYIAVYDDTQPLRFDSDAALPRMEPRFPWVEQGPQYW 60
Db 25 GSHSMYFYTSVRGPGPRFISVGYDDTQVRFDSDAASPREPRAPWIEQGPETW 84
QY 61 EWTGTGAKANAQTRVALNMLRRYQSEAGSHLQMGNGCDMPGRLRLGYHQHAYDG 120
Db 85 DENTQICKTNTQTDRESLRNLGYYNQSEAGSHLQMGNGCDMPGRLRLGHQNPAYDG 144
QY 121 KDVISNELRLSWTAADTVAQITQRYEAEVEEPTVLEGBCLELLRLRYLNGKXETLQ 180
Db 145 KDVIALLNEDLSWTAADTVAQITQRYEAEVEEPTVLEGBCLELLRLRYLNGKXETLQ 204
QY 181 RADPPKXAHVAHPISDHEATLRCWALGFYPAETITLWQDGEQTOCTELVETRPAGDGT 240
Db 205 RADPPKXTHVHPISDHEATLRCWALGFYPAETITLWQDGEQTOCTELVETRPAGDRT 264
QY 241 FOKAAVVPVSGEQRVTCVQHEGPPQPLILRW 274
Db 265 FOKAAVVPVSGEQRVTCVQHEGPPKPLILRW 298

RESULT 7
1B67 HUMAN STANDARD; PRT; 362 AA.
AC Q29836; Q29678; Q8NC5; Q951A6; Q9BD38;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-67 alpha chain precursor
GN (MHC class I antigen B*67).
OS HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*6701).
RX MEDLINE=34294981; Pubmed=7517584;
RA Little A.-M., Domena J.D., Hildebrand W.H., Shen S.Y., Barber L.D.,
RA Marsh S.G.E., Bias W.B., Parham P.;
RT "HLA-B*67: a member of the HLA-B*67 family that expresses the ME1
RT epitope.";
RL Tissue Antigens 43:38-43(1994).
RN [2]
RP SEQUENCE OF 26-205 FROM N.A. (B*6701).
RC TISSUE=Blood;
RA Peterdorff E.;
RT "Molecular diversity of HLA-B*67";
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (B*6702).
RA Iglehart B.A., Leffell W.S.;
RT "HLA-B*6702 (Promoter-3'UTR).";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

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RN [4]
RP SEQUENCE OF 26-206 FROM N.A. (B*6702).
RA Baldaasarte L.A., Hurley C.K.;
RT "Novel HLA-B allele (HLA-B*67012 variant)";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- POLYMORPHISM: The following alleles of B-67 are known: B*6701
CC (B-67LAV) and B*6702. The sequence shown is that of B*6701.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; L17005; AAC37548.1; -
DR EMBL; U18789; AAB60360.1; -
DR EMBL; AF487379; AAL93257.1; -
DR EMBL; AF321835; AAK09378.1; -
DR EMBL; AF321834; AAK09378.1; JOINED.
DR EMBL; AY050196; AAL18235.1; -
DR EMBL; AY050195; AAL18235.1; JOINED.
DR PIR; I59645; I59645.
DR HSSP; P30460; 1AGD.
DR Genew; HGNC:4932; HLA-B.
DR MIM; 142830; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001039; MHC I.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PF00129; MHC I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-67 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110 CYTOPLASMIC TAIL.
FT DISULFID 125 188 N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT DISULFID 227 283 BY SIMILARITY.
FT VARIANT 69 69 E--> G (in allele B*6702).
FT VARIANT 76 76 I--> V (in allele B*6702).
FT VARIANT 87 87 N--> E (in allele B*6702).
FT VARIANT 90 90 /FTID=VAR_016537.
FT VARIANT 93 93 /FTID=VAR_016538.
FT VARIANT 97 97 I--> K (in allele B*6702).
FT VARIANT 99 99 /FTID=VAR_016539.
FT VARIANT 100 100 A--> R (in allele B*6702).
FT VARIANT 100 100 T--> A (in allele B*6702).
FT VARIANT 100 100 /FTID=VAR_016541.
FT VARIANT 100 100 E--> V (in allele B*6702).
FT SEQUENCE 362 AA; 40342 MW; 3F6A17FC10230F70 CRC64;
SQ SEQUENCE 362 AA; 40342 MW; 3F6A17FC10230F70 CRC64;

Query Match 82.0%; Score 1227; DB 1; Length 362;

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Best Local Similarity	82.1%;	Pred. No. 1.7e-91;	
Matches	225;	Conservative	19; Mismatches 31; Indels 0; Gaps 0;
Qy	1	GSHSLRPFSTAVSPGCGEPRRYTAVYVDVDTQFLRPDSDAALPRMEPRPWEQGPQYW	60
Ddb	25	GSHSMRYFTYTSVRPGGEPFRFTSVGVVDVDTQFVRFDSDAASPREPRAPWIEQGEFYW	84
Qy	61	EWTTGYAKANAQTDVVALRNLLRRYVNSAGSHTLQGMNGCDMGDPGLLRGYTHQHYDG	120
Ddb	85	DRNTQYIYKAQAQTDRESLRNLRGVYVNSAGSHTLQRMVYCDVGPDGLLRGHNQFAYDG	144
Qy	121	KOYISLNEEDLSWTAAATVTAQIITQRYEAEVEAEERFTYLEGCELELLRRYLENGKETLQ	180
Ddb	145	KDYTALNEEDLSWTAAATVTAQIITQRYEAEVEAEERFTYLEGCELELLRRYLENGKETLQ	204
Qy	181	RADPPKARVAHPHPSDHEATLRCAWLGIFYPAEITLTWQDGEQQTDELVELVETRPAGDGT	240
Ddb	205	RADPPKTHVTHHPISDHEATLRCAWLGIFYPAEITLTWQDGEDQTDDELVELVETRPAGDRT	264
Qy	241	FOKWAAVVVPSSGEQRYTCHVQHEGLDPOPLILRW	274
Ddb	265	FOKWAAVVVPSSGEQRYTCHVQHEGLPKPLTLRW	298
RESULT 8			
1B73 HUMAN			
ID	1B73 HUMAN	STANDARD;	PRT; 363 AA.
AC	Q31612;		
DT	10-OCT-2003 (Rel. 42, Created)		
DT	10-OCT-2003 (Rel. 42, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	HLA class I histocompatibility antigen, B-73 alpha chain precursor		
DE	(MHC class I antigen B*73).		
GN	HLA-B OR HLAB.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
RN	SEQUENCE FROM N.A. (B*7301).		
RX	MEDLINE=95026796; PubMed=7524186;		
RA	Parham P., Arnett K.B., Adams E.J., Barber L.D., Domena J.D.,		
RA	Stewart D., Hildebrand W.H., Little A.-M.;		
RT	"The HLA-B*73 antigen has a most unusual structure that defines a		
RT	second lineage of HLA-B alleles";		
RL	Tissue Antigens 43:302-313(1994).		
RN	SEQUENCE FROM N.A. (B*7301).		
RX	MEDLINE=94299292; PubMed=7517915;		
RA	Vilches C., de Pablo R., Herrero M.J., Moreno M.E., Kreisler M.;		
RT	"HLA-B*73: an atypical HLA-B molecule carrying a Bw6-epitope motif		
RT	variant and a B pocket identical to HLA-B*27";		
RL	Immunogenetics 40:166-166(1994).		
RN	SEQUENCE FROM N.A. (B*7301).		
RX	MEDLINE=96164742; PubMed=8547229;		
RA	Hoffmann H.J., Kristensen T.J., Jensen T.G., Graugaard B., Lamm L.U.;		
RT	"Antigenic characteristics and cDNA sequences of HLA-B*73";		
RL	Eur. J. Immunogenet. 22:231-240(1995).		
RN	SEQUENCE FROM N.A. (B*7301).		
RX	TISSUE=Blood;		
RA	MEDLINE=22512041; PubMed=13622774;		
RA	Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,		
RA	Madrigal J.A., Little A.-M.;		
RT	"Cloning and sequencing full-length HLA-B and -C genes";		
RL	Tissue Antigens 63:20-48(2003)		
CC	- FUNCTION: Involved in the presentation of foreign antigens to the		
CC	immune system.		
CC	- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-		
CC	microglobulin).		
CC	- SUBCELLULAR LOCATION: Type I membrane protein.		

DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE HLA class I histocompatibility antigen, B-8 alpha chain precursor
 DE (MHC class I antigen B*8).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (B*0801).
 RX MEDLINE=89235215; PubMed=2715640;
 RA Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles";
 RL J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (B*0801).
 RX TISSUE=Blood;
 RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
 RT Madrigal J.A., Little A.-M.;
 RL "Cloning and sequencing full-length HLA-B and -C genes";
 RL Tissue Antigens 61:20-48(2003).
 RN [3]
 RP SEQUENCE FROM N.A. (B*0801).
 RA Shiina S., Tamiya G., Oka A., Inoko H.;
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 26-206 FROM N.A. (B*0804).
 RX MEDLINE=97473039; PubMed=9331954;
 RA Hoyer R.J., Bratlie A., Schreuder G.M., Hurley C.K.;
 RT "Characterization of a novel HLA-B allele, B*0804, in a Norwegian
 RL family";
 RL Tissue Antigens 50:308-310(1997).
 RN [5]
 RP SEQUENCE OF 33-257 FROM N.A. (B*0804).
 RA Eberle M., Lorentzen D., Iwanaga K.K., Watkins D.I.;
 RT "Identification of a new HLA-B*08 variant, B*08NEW";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 26-206 FROM N.A. (B*0806).
 RA Marcos C.Y., Lazaro A.M., Noreen H., Stastny P.;
 RT "New HLA-B locus allele";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 26-206 FROM N.A. (B*0807 AND B*0809).
 RX MEDLINE=20236861; PubMed=10777103;
 RA Kennedy C.T., Dodd R., Le T., Wallace R., Ng G., Greville W.D.,
 RA Kennedy A., Taverniti A., Moses J.H., Clow N., Watson N.,
 RA Dunkley H.;
 RT "Routine HLA-B genotyping with PCR-sequence-specific oligonucleotides
 RL (PCR-SSO) detects eight new alleles: B*0807, B*0809, B*3529,
 RL B*3532, B*4025, B*5304 and B*5508";
 RL Tissue Antigens 55:266-270(2000).
 RN [8]
 RP SEQUENCE OF 116-206 FROM N.A. (B*0809).
 RX MEDLINE=20166355; PubMed=10703615;
 RA Elsner H.A., Blasczyk R.;
 RT "Identification of the novel allele HLA-B*0809 in a Caucasian
 RL individual: estimation of allogeneic potential between B*08
 RL variants";
 RL Tissue Antigens 55:74-77(2000).
 RN [9]
 RP SEQUENCE OF 26-206 FROM N.A. (B*0809; B*0812; B*0813 AND B*0814).
 RX MEDLINE=21276061; PubMed=11380931;
 RA Steiner N.K., Gans C.P., Kosman C., Baldassarre L.A., Edson S.,
 RA Jones P.F., Rizzuto G., Pimthanotai N., Koester R., Milton W., Ng J.,
 RA Hartzman R.J., Hurley C.K.;
 RT "Novel HLA-B alleles associated with antigens in the 8C CREG";
 RL Tissue Antigens 57:373-375(2001).
 RN [10]
 RP SEQUENCE OF 26-206 FROM N.A. (B*0810).

RA Day S.;
 RT "A new B*08 variant allele";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 25-300.
 RX MEDLINE=97130420; PubMed=8976183;
 RA Reid S.W., McAdam S., Smith K.J., Klennerman P., O'Callaghan C.A.,
 RA Harlos K., Jacobsen B.K., McMichael A.J., Bell J.I., Stuart D.I.,
 RA Jones E.Y.;
 RT "Antagonist HIV-1 Gag peptides induce structural changes in HLA B8";
 RL J. Exp. Med. 184:2279-2286(1996).
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- POLYMORPHISM: The following alleles of B-8 are known: B*0801,
 CC B*0804, B*0806, B*0807 (B*NV), B*0809 (B*HM), B*0810,
 CC B*0812, B*0813 and B*0814. The sequence shown is B*0801.
 CC -----
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 DR EMBL; M24036; AAA52662.1; -
 DR EMBL; AJ295294; CAC18876.1; -
 DR EMBL; AP000507; BAB63309.1; -
 DR EMBL; U67331; AAB07726.1; -
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 DR EMBL; U74386; AAB41720.1; -
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 DR EMBL; AF056483; AAC14124.1; JOINED.
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 DR EMBL; AF127248; AAD31431.1; -
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 DR EMBL; AF102559; AAD28165.1; JOINED.
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 DR EMBL; AF226150; AAF36681.1; JOINED.
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 DR EMBL; AF310144; AAG27470.1; JOINED.
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 DR EMBL; AY016211; AAK38401.1; JOINED.
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 DR EMBL; AJ133102; CAB38945.1; JOINED.
 DR PIR; I84431; I84431.
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 DR PDB; IAGL; 04-FEB-03.
 DR PDB; IAGM; 04-FEB-03.
 DR PDB; IAGN; 04-FEB-03.
 DR PDB; IAGO; 04-FEB-03.
 DR PDB; IAGP; 04-FEB-03.
 DR PDB; IAGQ; 04-FEB-03.
 DR PDB; IAGR; 04-FEB-03.
 DR PDB; IAGS; 04-FEB-03.
 DR PDB; IAGT; 04-FEB-03.
 DR PDB; IAGU; 04-FEB-03.
 DR PDB; IAGV; 04-FEB-03.
 DR PDB; IAGW; 04-FEB-03.
 DR PDB; IAGX; 04-FEB-03.
 DR PDB; IAGY; 04-FEB-03.
 DR PDB; IAGZ; 04-FEB-03.
 DR PDB; IAGA; 04-FEB-03.
 DR PDB; IAGB; 04-FEB-03.
 DR PDB; IAGC; 04-FEB-03.
 DR PDB; IAGD; 04-FEB-03.
 DR PDB; IAGE; 04-FEB-03

[illegible][illegible]

```
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-42 ALPHA CHAIN
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT VARIANT 33 33
FT Y -> H (in allele B*4202).
FT /FTIG=VAR 016460.
FT SEQUENCE 362 AA; 40333 MW; C9155AB015DEA1BE CRC64;

Query Match 81.8%; Score 1224; DB 1; Length 362;
Best Local Similarity 81.4%; Pred. No. 2.9e-91;
Matches 223; Conservative 21; Mismatches 30; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGPRVIAVEYVDDTQFLRFSDDAALPRMEPRPVEQSGPYW 60
DB 25 GSHSMRYFTSVSRPGRGPRVIAVEYVDDTQFLRFSDDAALPRMEPRPVEQSGPYW 84
QY 61 EWTGTGAKANAQTDRLVALNRLRYNQSEAGSHTLQGMNGCDMGDPGRLRLRYHQHAYDG 120
DB 85 DRNTQIYKAAQTDRESLENLRYNQSEAGSHTLQGMNGCDMGDPGRLRLRYHQHAYDG 144
QY 121 KDYISLNEDLSRWTAAADTAQAQITQKWEAREABQLRAYLEGTQVWLRRLYENGKTLQ 180
DB 145 KDYIALNEDLSRWTAAADTAQAQITQKWEAREABQLRAYLEGTQVWLRRLYENGKTLQ 204
QY 181 RADPPKHAHVAHPISDHEATLRCWALGFYPABITLTWQDGEBOQTQDTLVETRPAGDGT 240
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPABITLTWQDGEBOQTQDTLVETRPAGDGT 264
QY 241 FOKWAAVVPSEGEORVYTCVHQHGLFQPLILRW 274
DB 265 FOKWAAVVPSEGEORVYTCVHQHGLFQPLILRW 298

RESULT 11
1B01 GORGO STANDARD; PRT; 362 AA.
AC P30379;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Class I histocompatibility antigen, GOGO-B0101 alpha chain precursor.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92078650; PubMed=1744581;
RA Lawlor D.A., Warren E., Taylor P., Parham P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
RL J. Exp. Med. 174:1491-1509(1991).
CC -I- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
CC -I- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
CC -----
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CC -----
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EMBL; X60255; CAA42807.1; -.
PIR: JH0539; JH0539.
HSP: P03989; IJSA.
InterPro: IPR007110; Ig-like.
InterPro: IPR003597; Ig_cl.
InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR PRINTS: PR01638; MHCCLASSI.
DR PRODOM: PD000050; MHC_I; 1.
DR SMART: SMO0407; IGCI; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT GOGO-B0101 ALPHA CHAIN.
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT SEQUENCE 362 AA; 40170 MW; 419EE29817165A4 CRC64;

Query Match 81.8%; Score 1223; DB 1; Length 362;
Best Local Similarity 81.8%; Pred. No. 3.5e-91;
Matches 224; Conservative 17; Mismatches 33; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGPRVIAVEYVDDTQFLRFSDDAALPRMEPRPVEQSGPYW 60
DB 25 GSHSMRYFTSVSRPGRGPRVIAVEYVDDTQFLRFSDDAALPRMEPRPVEQSGPYW 84
QY 61 EWTGTGAKANAQTDRLVALNRLRYNQSEAGSHTLQGMNGCDMGDPGRLRLRYHQHAYDG 120
DB 85 DRETQTSKAQAQTDRENLRLRYNQSEAGSHTLQGMNGCDMGDPGRLRLRYHQHAYDG 144
QY 121 KDYISLNEDLSRWTAAADTAQAQITQKWEAREABQLRAYLEGTQVWLRRLYENGKTLQ 180
DB 145 KDYIALNEDLSRWTAAADTAQAQITQKWEAREABQLRAYLEGTQVWLRRLYENGKTLQ 204
QY 181 RADPPKHAHVAHPISDHEATLRCWALGFYPABITLTWQDGEBOQTQDTLVETRPAGDGT 240
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPABITLTWQDGEBOQTQDTLVETRPAGDGT 264
QY 241 FOKWAAVVPSEGEORVYTCVHQHGLFQPLILRW 274
DB 265 FOKWAAVVPSEGEORVYTCVHQHGLFQPLILRW 298

RESULT 12
1B47 HUMAN STANDARD; PRT; 362 AA.
ID 1B47 HUMAN STANDARD; PRT; 362 AA.
AC P30485; O19555; O77933; Q95392; Q9GIL3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Class I histocompatibility antigen, B-47 alpha chain precursor.
DE HLA class I histocompatibility antigen, B-47 alpha chain precursor (MHC class I antigen B*47) (Bw-47).
DE HLA-B OR HLAB.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*4701).
RX MEDLINE=88152906; PubMed=3257938;
RA Zemour J., Ennis P.D., Parham P., Dupont B.;
RT "Comparison of the structure of HLA-Bw47 to HLA-B13 and its
```


RP SEQUENCE OF 26-206 FROM N.A. (A*2304 AND A*2305).
RX MEDLINE=21068830; PubMed=11169246;
RA Steiner N.K., Edson S.M., Mitten W., Ng J., Hartzman R.J.,
RA Hurley C.K.; HLA-A alleles carry previously observed polymorphisms.;
RT Tissue Antigens 56:551-552(2000).
RL Tissue Antigens 56:551-552(2000).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to
CC the immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- POLYMORPHISM: The following alleles of A-23 are known: A*2301,
CC A*2302, A*2303, A*2304 and A*2305. The sequence shown is that of
CC A*2301.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M64742; AAA03662.1; -;
DR EMBL; AF137080; AAD33736.1; -;
DR EMBL; AF137079; AAD33736.1; JOINED.
DR EMBL; AF102572; AAD28171.1; -;
DR EMBL; AF102571; AAD28171.1; JOINED.
DR EMBL; AF135549; AAD22272.1; -;
DR EMBL; AF135548; AAD22272.1; JOINED.
DR EMBL; AF140860; AAD31878.1; -;
DR EMBL; AF140859; AAD31878.1; JOINED.
DR HSP; Q95352; IHKK.
DR Genew; HGNC:4931; HLA-A.
DR MIM; 142800; -;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF0047; IG; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PR01638; MHCCLASS1.
DR ProDom; PD000050; MHC I; 1.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-23 ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332
FT CONNECTING PEPTIDE.
FT CYTOPLASMIC TAIL.
FT N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT BY SIMILARITY.
FT Y -> C (in allele A*2305).
FT /FTID=VAR 016606.
FT K -> N (in allele A*2303).
FT /FTID=VAR 016607.
FT L -> W (in allele A*2302).
FT /FTID=VAR 016608.
FT DG -> EW (in allele A*2304).
FT /FTID=VAR 016609.
FT VARIANT 31 31
FT VARIANT 151 151
FT VARIANT 180 180
FT VARIANT 190 191
FT VARIANT 365 AA; 40732 MW; C372DE503BF393D0 CRC64;
SQ SEQUENCE 365 AA; 40732 MW; C372DE503BF393D0 CRC64;
Query Match 81.8%; Score 1223; DB 1; Length 365;
Best Local Similarity 81.4%; Pred. No. 3 6e-91;
Matches 223; Conservative 32; Indels 0; Gaps 0;

QY 1 GSHSLRYFTAVSRPGRGEPRIYAVYVDOTQFLRFDSDAAIPRMEPRPFWVQEGQY 60
DB 25 GSHSMRYFTSVSRPGRGEPRIYAVYVDOTQFLRFDSDAAIPRMEPRPFWVQEGQY 84
QY 61 EWTGTYAKANAQDRVALRNLLRYNQSEAGSHTLQMGNGCDMGDPGRLRLRGYHQYADG 120
DB 85 DEETGKVAHSQTDRENRLRLRYNQSEAGSHTLQMGFCDDVSGDGRFLRGYHQYADG 144
QY 121 KDYISLNEJRSWTAADTVAQITQRFYAEYAEFFTYLEGSCLELLRRLYENGKETLQ 180
DB 145 KDYIALKEDJRSWTAADMAAQITQKWEARVAEQRLAYLEGTCDVGLRRLYENGKETLQ 204
QY 181 RADPPKAAVHHPISDHEATLRWALGFYPAETITLTWQRDGEQOTQDTLVEYTRPAGDGT 240
DB 205 RTDPPKTHMTHHPISDHEATLRWALGFYPAETITLTWQRDGEQOTQDTLVEYTRPAGDGT 264
QY 241 FQKWAADVVSFGEEQRYTCHVQHEGLPQPLILRW 274
DB 265 FQKWAADVVSFGEEQRYTCHVQHEGLPQPLILRW 298

RESULT 14
1B37 HUMAN
ID 1B37 HUMAN STANDARD; PRT; 362 AA.
AC P18453; O19627; Q95HA3; Q95HA8; Q95HM9; Q9GJ31;
DT 01-NOV-1990 (Rel. 15, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B*37 alpha chain precursor
DE (MHC class I antigen B*37).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A. (B*3701).
RX MEDLINE=90207291; PubMed=2320591;
RA Ennis P.D., Zemmour J., Salter R.D., Parham P.;
RT "Rapid cloning of HLA-A,B CDNA by using the polymerase chain
RT reaction: frequency and nature of errors produced in amplification.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
[2]
RP SEQUENCE FROM N.A. (B*3704).
RC TISSUE=Peripheral blood;
RX MEDLINE=22025782; PubMed=12028544;
RA Estefania E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.;
RT "Complementary DNA sequence of the novel HLA-B*3704 allele.";
RL Tissue Antigens 59:142-144(2002).
[3]
RP SEQUENCE FROM N.A. (B*3705).
RX MEDLINE=22131942; PubMed=12135437;
RA Pyo C.-W., Han H., Kim T.G.;
RT "Identification of a new HLA-B allele, B*3705 containing a Bw6
RT sequence motif.";
RL Tissue Antigens 59:335-337(2002).
[4]
RP SEQUENCE OF 1-322 FROM N.A. (B*3701).
RA Hurley C.K., Bei M., Rodriguez S., Johnson A.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE OF 26-206 FROM N.A. (B*3704).
RA Gans C.P., Hurley C.K.;
RT "Novel HLA-B allele.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- POLYMORPHISM: The following alleles of B*37 are known: B*3701,
CC B*3704 and B*3705. The sequence shown is that of B*3701.

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CC -----
 DR ENBL; M32320; AAA36233.1; --
 DR ENBL; AF389378; AAL26324.1; --
 DR ENBL; AF418978; AAL07502.1; --
 DR ENBL; AF284828; AAK82990.1; --
 DR ENBL; AF284826; AAK82990.1; JOINED.
 DR ENBL; AF284827; AAK82990.1; JOINED.
 DR ENBL; U11267; AAA19927.1; --
 DR ENBL; AF303102; AAG21400.1; --
 DR ENBL; AF303101; AAG21400.1; JOINED.
 DR PIR; C35997; C35997.
 DR HSP; HGNC:4932; HLA-B.
 DR MIM; 142830; --
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT -----
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT VARIANT 104 104
 FT VARIANT 106 107
 FT VARIANT 195 195
 FT VARIANT 195 195
 FT VARIANT 362 AA; 40456 MW; FAB4375P05474725 CRC64;
 SQ SEQUENCE 362 AA; 40456 MW; FAB4375P05474725 CRC64;
 Query Match 81.7%; Score 1222; DB 1; Length 362;
 Best Local Similarity 81.4%; Pred. No. 4.3e-91;
 Matches 223; Conservative 19; Mismatches 32; Indels 0; Gaps 0;

Qy 1 GSHSLRFSTAVSRGEGEPRYIAVEYVDDTQVRFDSDAALPRMEPRPWEQGPQYW 60
 Db 25 GSHSMRYFHTSVSRGEGEPRFISGVYDDTQVRFDSDAASPRPWEQGPQYW 84
 Qy 61 EWTGYKANAQTDVVALNLLRYNQSEASHYLOQMNGCDMGPDGRLRLGYHQYADG 120
 Db 85 DRETQISKNTQTYREDLRTLLRYNQSEASHYLOQMNGCDMGPDGRLRLGYNQFAYDG 144
 Qy 121 KDYSLNEDLRSTAAQDTVAQITQRFYAEYAEPRFYLEGCELELLRYLNGKETLQ 180
 Db 145 KDYLALNEDLSSTAAQDTVAQITQRFYAEYAEPRFYLEGCELELLRYLNGKETLQ 204
 Qy 181 RADPKKVAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEPRPADGDT 240
 Db 205 RADPKKTHVTHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEPRPADGRT 264

Qy 241 FQKWAAVVPSEGEQRYTCHVQHEGLPQPLIRW 274
 Db 265 FQKWAAVVPSEGEQRYTCHVQHEGLPQPLIRW 298

RESULT 15

ID 1B02 GORGO STANDARD; PRT; 362 AA.
 AC P30380;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Class I histocompatibility antigen, GOGO-B0102 alpha chain precursor.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OX NCBI_TaxID=9595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92078860; PubMed=1744581;
 RA Lawlor D.A., Warren E., Taylor P., Parham P.;
 RT "Gorilla class I major histocompatibility complex alleles: comparison
 RT to human and chimpanzee class I.";
 RL J. Exp. Med. 174:1491-1509(1991).
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
 CC immune system.
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
 CC microglobulin).
 CC -----
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CC -----
 CC EMBL; X60693; CAA43101.1; --
 DR PIR; JH0540; JH0540.
 DR HSP; P03988; ILSA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT -----
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CARBOHYD 110 110
 SQ SEQUENCE 362 AA; 40204 MW; E19EE82B7CC7BECD CRC64;
 Query Match 81.6%; Score 1221; DB 1; Length 362;
 Best Local Similarity 81.8%; Pred. No. 5.1e-91;
 Matches 224; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GSHSLRFSTAVSRGEGEPRYIAVEYVDDTQVRFDSDAALPRMEPRPWEQGPQYW 60
 Db 25 GSHSMRYFHTSVSRGEGEPRFISGVYDDTQVRFDSDAASPRPWEQGPQYW 84

Qy	61	BWTTGYAKAQTDRVALRNLRLRYNOSAGSHTLQCMNGCDMPDGRLLRGYHQHAYDG	120
Db	85	DRETQTSKAQAQTDRNLRIRIALRYNOSAGSHTFQRMFGCDVQPDGELLRGYSQSAVDG	144
Qy	121	KDYISLNEDELSWTAADTVAQITQRFYEAEEYAEFEFTYLEGECLELLRRYLENGKETLQ	180
Db	145	KDYIALNEDELSWTAADTAQAQITQKWEAAREAQRLRAYLEGTCEVWLRYLENGRETQ	204
Qy	181	RADPEKAHVAHHPISDHEATLRCWALGFYPAEITLTTWODGEEOTQDTLVETRPAGDGT	240
Db	205	RADTFKTHVTHHPISDHEATLRCWALGFYPAEITLTTWODGEDQIQDTLVETRPAGDGT	264
Qy	241	FKWAAVVVPSGEBQRYTCHVQHEGLPQPLIRW	274
Db	265	FKWAAVVVPSGEBEERYTCHVQHEGLPKPLIRW	298

Search completed: June 18, 2004, 19:25:59
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:22:16 ; Search time 45 Seconds
(without alignments)
1921.155 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 1496

Sequence: 1 GSHSLRFVSTAVSRGRGP.....QRYTCHVQHEGLPOPLLRW 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

- 1: sp archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1496	100.0	324	7	Q861F0	Q861f0 homo sapien
2	1496	100.0	324	7	Q861E9	Q861e9 homo sapien
3	1496	100.0	346	7	Q8WLP5	Q8wlp5 homo sapien
4	1496	100.0	442	7	Q9SHC0	Q9shc0 homo sapien
5	1491	99.7	346	7	Q8MGC1	Q8mgc1 homo sapien
6	1491	99.7	362	7	Q9TP68	Q9tp68 homo sapien
7	1477	98.7	346	7	Q95IT2	Q95it2 pan troglod
8	1477	98.7	362	6	Q7YR27	Q7yr27 pan troglod
9	1240	82.9	274	7	O19692	O19692 homo sapien
10	1240	82.9	362	7	P79612	P79612 homo sapien
11	1240	82.9	362	7	Q78189	Q78189 homo sapien
12	1239	82.8	362	4	Q29705	Q29705 homo sapien
13	1237	82.7	354	7	Q9MW41	Q9mw41 macaca mula
14	1237	82.7	362	7	Q9MXK1	Q9mxk1 pan troglod
15	1236	82.6	359	7	Q29934	Q29934 homo sapien
16	1235	82.6	362	7	Q9MXI2	Q9mxI2 pan troglod

17	1234	82.5	273	7	Q8SNC9	Q8snc9 homo sapien
18	1234	82.5	341	7	O19589	O19589 homo sapien
19	1234	82.5	362	7	Q9MXD1	Q9mxd1 pan troglod
20	1233	82.4	362	7	Q860I7	Q860i7 homo sapien
21	1232	82.4	298	7	Q9GJF1	Q9gjf1 homo sapien
22	1232	82.4	362	7	Q9TPW6	Q9tpw6 homo sapien
23	1232	82.4	362	7	Q7YQ80	Q7yq80 homo sapien
24	1230	82.2	363	7	Q8MEG3	Q8meg3 pan troglod
25	1228	82.1	354	7	O95530	O95530 pan troglod
26	1228	82.1	362	7	Q9MXI0	Q9mxI0 pan troglod
27	1228	82.1	362	7	Q9MXL8	Q9mxL8 pan troglod
28	1227	82.0	359	7	Q30711	Q30711 macaca mula
29	1227	82.0	363	7	Q30988	Q30988 pan troglod
30	1225	81.9	365	7	Q9TQ74	Q9tq74 homo sapien
31	1224	81.8	347	7	O9MWK1	O9mwk1 gorilla gor
32	1224	81.8	350	7	O19691	O19691 homo sapien
33	1224	81.8	362	7	Q9MXK5	Q9mxK5 pan troglod
34	1224	81.8	362	7	Q9MXM2	Q9mxM2 pan troglod
35	1224	81.8	362	7	Q9TFL5	Q9tfl5 pan troglod
36	1223	81.8	347	7	Q9MWK2	Q9mwk2 gorilla gor
37	1223	81.8	354	7	Q95412	Q95412 hylobates 1
38	1223	81.8	359	7	Q860F2	Q860f2 macaca neme
39	1223	81.8	362	7	Q29637	Q29637 homo sapien
40	1223	81.8	362	7	Q7YQ88	Q7yq88 homo sapien
41	1222	81.7	361	7	Q9GJ77	Q9gj77 macaca mula
42	1222	81.7	362	7	Q9MXK4	Q9mxK4 pan troglod
43	1222	81.7	362	7	Q30716	Q30716 macaca mula
44	1222	81.7	362	7	Q9GIX2	Q9gix2 homo sapien
45	1222	81.7	362	7	Q31602	Q31602 homo sapien

ALIGNMENTS

RESULT 1

Q861F0 ID Q861F0 PRELIMINARY; PRT; 324 AA.
AC Q861F0;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Nonclassical MHC class I antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. Xu L., Liu Y., Zeng Y.,
RA He X., Xu L., Liu Y., Zeng Y.,
RT "Nonclassical MHC class I HLA-F.",
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY216682; AAC37689.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 324 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;
Query Match 100.0%; Score 1496; DB 7; Length 324;

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Best Local Similarity 100.0%; Pred. No. 2.6e-122;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRSTAVSRPGRGEPYIAVEYDDTQFLRFSDAAIPRMEPRBPWVEQGPQYW 60
DB 18 GSHSLRSTAVSRPGRGEPYIAVEYDDTQFLRFSDAAIPRMEPRBPWVEQGPQYW 77
QY 61 EWTITGAKANAQTDRAVALNLLRRYNSQSEAGSHTLQMGNCMDGPDGRLLRGYHQHAYDG 120
DB 78 EWTITGAKANAQTDRAVALNLLRRYNSQSEAGSHTLQMGNCMDGPDGRLLRGYHQHAYDG 137
QY 121 KYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFRYLGECELELLRRYLENGKETLQ 180
DB 138 KYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFRYLGECELELLRRYLENGKETLQ 197
QY 181 RADPPKARVAHPISDHEATLRWALGFYPAEITLTWQRDGEEOQTDTLVEVTRPAGDGT 240
DB 198 RADPPKARVAHPISDHEATLRWALGFYPAEITLTWQRDGEEOQTDTLVEVTRPAGDGT 257
QY 241 FQKMAAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
DB 258 FQKMAAVVPSGEEQRYTCHVQHEGLPQPLILRW 291

RESULT 2
Q861E9 PRELIMINARY; PRT; 324 AA.
AC Q861E9;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Xu L., Zeng Y., He X.;
RT "A new polymorphism in non-classical MHC class I HLA-F.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY221102; AAO34407.1; -
DR GO; GO:0016020; C:membrane response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I.
DR SMART; SM00407; IGC1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D271674 CRC64;

Query Match 100.0%; Score 1496; DB 7; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.6e-122;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRSTAVSRPGRGEPYIAVEYDDTQFLRFSDAAIPRMEPRBPWVEQGPQYW 60
DB 18 GSHSLRSTAVSRPGRGEPYIAVEYDDTQFLRFSDAAIPRMEPRBPWVEQGPQYW 77
QY 61 EWTITGAKANAQTDRAVALNLLRRYNSQSEAGSHTLQMGNCMDGPDGRLLRGYHQHAYDG 120
DB 78 EWTITGAKANAQTDRAVALNLLRRYNSQSEAGSHTLQMGNCMDGPDGRLLRGYHQHAYDG 137

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QY 121 KYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFRYLGECELELLRRYLENGKETLQ 180
DB 138 KYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFRYLGECELELLRRYLENGKETLQ 197
QY 181 RADPPKARVAHPISDHEATLRWALGFYPAEITLTWQRDGEEOQTDTLVEVTRPAGDGT 240
DB 198 RADPPKARVAHPISDHEATLRWALGFYPAEITLTWQRDGEEOQTDTLVEVTRPAGDGT 257
QY 241 FQKMAAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
DB 258 FQKMAAVVPSGEEQRYTCHVQHEGLPQPLILRW 291

RESULT 3
Q8WLP5 PRELIMINARY; PRT; 346 AA.
AC Q8WLP5;
DT 01-WAR-2002 (TREMELrel. 20, Created)
DT 01-WAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE MHC class Ib antigen.
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation spanning the nonclassical class I genes.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA He X., Liu Y., Xu L., Zeng Y.;
RT "Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Liu Y., Zeng Y.;
RT "Cloning of full-length HLA-F*0101 variant 2 cDNA from Han Chinese.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF523285; AAM74980.1; -
DR EMBL; AF523286; AAM74981.1; -
DR EMBL; AF523287; AAM74982.1; -
DR EMBL; AF523288; AAM74983.1; -
DR EMBL; AF523289; AAM74984.1; -
DR EMBL; AF523290; AAM74985.1; -
DR EMBL; AF523293; AAM74988.1; -
DR EMBL; AF523294; AAM74989.1; -
DR EMBL; AF523295; AAM74990.1; -
DR EMBL; AF523296; AAM74991.1; -
DR EMBL; AF523297; AAM74992.1; -
DR EMBL; AY253269; AAO86773.1; -
DR EMBL; AY253270; AAO86774.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 100.0%; Score 1496; DB 7; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.9e-122;

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Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFSDAAIPRMEPREPWEQEGPOYW 60
DB 22 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFSDAAIPRMEPREPWEQEGPOYW 81
QY 61 EWTGTGAKANAQTDVALNRLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGTHQAYDG 120
DB 82 EWTGTGAKANAQTDVALNRLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGTHQAYDG 141
QY 121 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ 180
DB 142 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ 201
QY 181 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 240
DB 202 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 261
QY 241 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
DB 262 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 295
RESULT 4
Q95HCO PRELIMINARY; PRT; 442 AA.
ID AC Q95HCO
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to major histocompatibility complex, class I, F.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009260; AA009260.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0008955; P: immune response; IEA.
DR InterPro; IPR001064; CRYSTALLIN.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_MHC.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 442 AA; 50427 MW; 6459D3B5F4B5704A CRC64;
Query Match 100.0%; Score 1496; DB 7; Length 442;
Best Local Similarity 100.0%; Pred. No. 4, 1e-122;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFSDAAIPRMEPREPWEQEGPOYW 60
DB 22 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFSDAAIPRMEPREPWEQEGPOYW 81
QY 61 EWTGTGAKANAQTDVALNRLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGTHQAYDG 120
DB 82 EWTGTGAKANAQTDVALNRLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGTHQAYDG 141
QY 121 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ 180
DB 142 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ 201
QY 181 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 240
DB 202 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 261
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFSDAAIPRMEPREPWEQEGPOYW 60
DB 22 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFSDAAIPRMEPREPWEQEGPOYW 81
QY 61 EWTGTGAKANAQTDVALNRLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGTHQAYDG 120
DB 82 EWTGTGAKANAQTDVALNRLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGTHQAYDG 141
QY 121 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ 180
DB 142 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ 201
QY 181 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 240
DB 202 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 261
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142 KDYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ 201
181 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 240
202 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 261
241 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
262 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 295
RESULT 5
Q8MGQ1 PRELIMINARY; PRT; 346 AA.
ID AC Q8MGQ1
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MHC class Ib antigen.
GN HLA-F.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishitani A.; Miki A.; Williams L.M.; Moore Y.; Geraghty D.E.;
RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation spanning the nonclassical class I genes."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AF523284; AA074979.1; -.
DR EMBL; AF523291; AA074986.1; -.
DR EMBL; AF523292; AA074987.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR001064; CRYSTALLIN.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_MHC.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 346 AA; 39061 MW; D4782968A67E9B7D CRC64;
Query Match 99.7%; Score 1491; DB 7; Length 346;
Best Local Similarity 99.6%; Pred. No. 7, 9e-122;
Matches 273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFSDAAIPRMEPREPWEQEGPOYW 60
DB 22 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFSDAAIPRMEPREPWEQEGPOYW 81
QY 61 EWTGTGAKANAQTDVALNRLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGTHQAYDG 120
DB 82 EWTGTGAKANAQTDVALNRLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGTHQAYDG 141
QY 121 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ 180
DB 142 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ 201
QY 181 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 240
DB 202 RADPPKAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 261
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Db 202 RADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLTVETRPAGDGT 261
QY 241 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
Db 262 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

RESULT 6
Q9TP68 PRELIMINARY; PRT; 362 AA.
AC Q9TP68;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE D3377H14.9 (Major histocompatibility complex, class I, F
DE (CD412)).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AL022723; CAB4623.1; -.
DR HSP; Q30201; IAE2.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGCL1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40578 MW; 970D072C813A07E2 CRC64;

Query Match 99.7%; Score 1491; DB 7; Length 362;
Best Local Similarity 99.6%; Pred. No. 8.4e-12; Mismatches 1; Indels 0; Gaps 0;
Matches 273; Conservative 0;

QY 1 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 60
Db 22 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 81
QY 61 EWTGTYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDG 120
Db 82 EWTGTYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDG 141
QY 121 KDYISLNEDLSRWTAADVAQITQRFYEAEYAEFRYLEGECLLELLRRYLENGKETLQ 180
Db 142 KDYISLNEDLSRWTAADVAQITQRFYEAEYAEFRYLEGECLLELLRRYLENGKETLQ 201
QY 181 RADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLTVETRPAGDGT 240
Db 202 RADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLTVETRPAGDGT 261
QY 241 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
Db 262 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

RESULT 8
Q7YR27 PRELIMINARY; PRT; 362 AA.
AC Q7YR27;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Class ID.
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RESULT 7
Q95IT2 PRELIMINARY; PRT; 346 AA.
ID Q95IT2
AC Q95IT2;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE MHC class I antigen.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21291697; PubMed=11398964;
RA Adams E.J.; Farham P.;
RT "Genomic analysis of common chimpanzee major histocompatibility
RT complex class I genes.";
RL Immunogenetics 53:200-208(2001).
DR EMBL; AF338355; AAK77479.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGCL1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;

Query Match 98.7%; Score 1477; DB 7; Length 346;
Best Local Similarity 99.3%; Pred. No. 1.3e-12;
Matches 272; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 60
Db 22 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 81
QY 61 EWTGTYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDG 120
Db 82 EWTGTYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQHAYDG 141
QY 121 KDYISLNEDLSRWTAADVAQITQRFYEAEYAEFRYLEGECLLELLRRYLENGKETLQ 180
Db 142 KDYISLNEDLSRWTAADVAQITQRFYEAEYAEFRYLEGECLLELLRRYLENGKETLQ 201
QY 181 RADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLTVETRPAGDGT 240
Db 202 RADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLTVETRPAGDGT 261
QY 241 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
Db 262 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

RESULT 8
Q7YR27 PRELIMINARY; PRT; 362 AA.
AC Q7YR27;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Class ID.
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GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22709134; PubMed=12799463;
RA Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA Yamagata T., Kuleki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT "Comparative sequencing of human and chimpanzee MHC class I regions
RT unveils insertions/deletions as the major path to genomic
RT divergence."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713 (2003).
DR EMBL; AB100087; BAC78191.1; -.
SQ SEQUENCE 362 AA; 40625 NW; BA5699D08181A1FF CRC64;

Query Match 98.7%; Score 1477; DB 6; Length 362;
Best Local Similarity 99.3%; Pred. No. 1.4e-120; Indels 0; Gaps 0;
Matches 272; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGRGEPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYW 60
DB 22 GSHSLRYFSTAVSRGGRGEPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYW 81
QY 61 EHTTGYAKANAQTDRAVALNLLRRYNOSEAGSHTLQMGNGCDMGDPGRLRGYHQA YDG 120
DB 82 EHTTGYAKANAQTDRAVALNLLRRYNOSEAGSHTLQMGNGCDMGDPGRLRGYHQA YDG 141
QY 121 KYIISLNEDLRSWTAADTVAQITQRFYEAEEYAEAEFRYVLEGECLLELLRRYLENGKETLQ 180
DB 142 KYIISLNEDLRSWTAADTVAQITQRFYEAEEYAEAEFRYVLEGECLLELLRRYLENGKETLQ 201
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPABITLTWQDGEQQTDELVELTRPAGDGT 240
DB 202 RADPPKARVAHPISDHEATLRCWALGFYPABITLTWQDGEQQTDELVELTRPAGDGT 261
QY 241 FOKWAAVVPSGEGEORYTCHVQHEGLPQPLILRW 274
DB 262 FOKWAAVVPSGEGEORYTCHVQHEGLPQPLILRW 295

RESULT 9
O19692 PRELIMINARY; PRT; 274 AA.
ID O19692
AC O19692;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HLA-B protein (Fragment).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87009855; PubMed=3489755;
RA Coppin H.L., McDavitt H.O.;
RT "Absence of polymorphism between HLA-B*27 genomic exon sequences
RT isolated from normal donors and ankylosing spondylitis patients.";
RL J. Immunol. 137:2168-2172 (1986).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; M14013; AAA59643.1; -.
DR HSSP; P03989; 1HSA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
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DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl_1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON TER 1
FT NON TER 274
SQ SEQUENCE 274 AA; 31659 MW; 0C9A7A4902383219 CRC64;

Query Match 82.9%; Score 1240; DB 7; Length 274;
Best Local Similarity 82.8%; Pred. No. 4.6e-100;
Matches 227; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGRGEPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYW 60
DB 1 GSHSLRYFSTAVSRGGRGEPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYW 60
QY 61 EHTTGYAKANAQTDRAVALNLLRRYNOSEAGSHTLQMGNGCDMGDPGRLRGYHQA YDG 120
DB 61 DRETQICAKAQTDREDLRLRLRYNOSEAGSHTLQMGNGCDMGDPGRLRGYHQA YDG 120
QY 121 KYIISLNEDLRSWTAADTVAQITQRFYEAEEYAEAEFRYVLEGECLLELLRRYLENGKETLQ 180
DB 121 KYIISLNEDLRSWTAADTVAQITQRFYEAEEYAEAEFRYVLEGECLLELLRRYLENGKETLQ 180
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPABITLTWQDGEQQTDELVELTRPAGDGT 240
DB 181 RADPPKARVAHPISDHEATLRCWALGFYPABITLTWQDGEQQTDELVELTRPAGDGT 240
QY 241 FOKWAAVVPSGEGEORYTCHVQHEGLPQPLILRW 274
DB 241 FOKWAAVVPSGEGEORYTCHVQHEGLPQPLILRW 274

RESULT 10
P79612 PRELIMINARY; PRT; 362 AA.
ID P79612
AC P79612;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HLA-B protein.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood.
RA Hasegawa T., Sugahara Y., Moriyama Y., Nanzai H., Ogawa A., Tawara K.,
RA Kondo S., Tokunaga K.;
RT "Molecular characterization of a novel HLA-B*27 allele.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; D83043; BAAL1753.1; -.
DR HSSP; P03989; 1HSA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
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DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 4041 MW; 3CA5547E65FDF84 CRC64;

Query Match      82.9%; Score 1240; DB 7; Length 362;
Best Local Similarity 82.5%; Pred. No. 6.8e-100;
Matches 226; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYDDTQFLRFSDSAAIPRMEPREPWVEQGPQYW 60
DB 25 GSHSMRYFHTSVSRPGRGEPRIYGVYDDTLFVRFSDSAAAPRMEPREPWVEQGPQYW 84

QY 61 EWTTCYAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDVGPGRLLRGHNGKQYDG 120
DB 85 DRETQICKAKAQTDRLSLRTLLRRYNQSEAGSHTLQSMYGCVDVGPGRLLRGHNGKQYDG 144

QY 121 KOYISLNEDLSRTAAADTAQITQRFYAEAYAEPRTYLGECELELLRRYLENGKETLQ 180
DB 145 KOYIALNEDLSRTAAADTAQITQKWEAAARVAEQRLAYLGECEVSWLRRYLENGKETLQ 204

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEPRAGDGT 240
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEPRAGDRT 264

QY 241 FQKWAAVVPSGEGEORYTCHVQHEGLPOPLILRW 274
DB 265 FQKWAAVVPSGEGEORYTCHVQHEGLPKPLTLRW 298

RESULT 11
Q78189 PRELIMINARY; PRT; 362 AA.
AC Q78189;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE MHC class I antigen.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98427840; PubMed=9756409;
RA Seurynck K., Baxter-Lowe L.A.;
RT "Novel polymorphism detected in exon 1 of HLA-B*2713."
RL Tissue Antigens 52:187-189(1998).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY). AND A BETA CHAIN (BETA-2-
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; AF026218; AAC42275.1; -.
DR HSSP; P03989; IHS.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.

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SQ SEQUENCE 362 AA; 40486 MW; BCO0FC372955711D CRC64;

Query Match      82.9%; Score 1240; DB 7; Length 362;
Best Local Similarity 82.8%; Pred. No. 6.8e-100;
Matches 227; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYDDTQFLRFSDSAAIPRMEPREPWVEQGPQYW 60
DB 25 GSHSMRYFHTSVSRPGRGEPRIYGVYDDTLFVRFSDSAAAPRMEPREPWVEQGPQYW 84

QY 61 EWTTCYAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDVGPGRLLRGHNGKQYDG 120
DB 85 DRETQICKAKAQTDRLSLRTLLRRYNQSEAGSHTLQMGNGCDVGPGRLLRGHNGKQYDG 144

QY 121 KOYISLNEDLSRTAAADTAQITQRFYAEAYAEPRTYLGECELELLRRYLENGKETLQ 180
DB 145 KOYIALNEDLSRTAAADTAQITQKWEAAARVAEQRLAYLGECEVSWLRRYLENGKETLQ 204

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEPRAGDGT 240
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEPRAGDRT 264

QY 241 FQKWAAVVPSGEGEORYTCHVQHEGLPOPLILRW 274
DB 265 FQKWAAVVPSGEGEORYTCHVQHEGLPKPLTLRW 298

RESULT 12
Q29705 PRELIMINARY; PRT; 362 AA.
AC Q29705;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE MHC class I antigen HLA-B precursor.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Balas A., Santos S., Vicario J.L.;
RT "Serological and molecular characterization of a novel HLA-B allele."
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U31971; AAA98506.1; -.
DR HSSP; P03989; IHS.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 362 AA; 40479 MW; 148B5656159EA505 CRC64;

Query Match      82.8%; Score 1239; DB 4; Length 362;
Best Local Similarity 82.5%; Pred. No. 8.3e-100;
Matches 226; Conservative 16; Mismatches 32; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYDDTQFLRFSDSAAIPRMEPREPWVEQGPQYW 60
DB 25 GSHSMRYFHTSVSRPGRGEPRIYGVYDDTLFVRFSDSAAAPRMEPREPWVEQGPQYW 84

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QY 61 EWTGYAKANAQTRVALNRLLRRYNNQSEAGSHLTQMGNGCDMPDGRLLRGYHQAIDG 120
DB 85 DRETQISKTNTQTVREDLRLTLRLRYNNQSEAGSHLTQMGNGCDMPDGRLLRGYHQAIDG 144
QY 121 KDYISLNEDLSWTAADTVAQITQRFVEAEYAEERFYLEGECLELLRRYLENGKETLQ 180
DB 145 KDYIALNEDLSWTAADTVAQITQRFVEAEYAEERFYLEGECLELLRRYLENGKETLQ 204
QY 181 RADPPKAAHVAHPISDHEATLRCWALGFYPABITLTWQDGEQDTQDTLVELTRPAGDGT 240
DB 205 RADPPKTHVTHPIPSDHEATLRCWALGFYPABITLTWQDGEQDTQDTLVELTRPAGDGT 264
QY 241 FQKWAUVVPSGEQRYTCHVQHEGLPOPLILRW 274
DB 265 FQKWAUVVPSGEQRYTCHVQHEGLPKPLTLRW 298

RESULT 13
Q9MW41 PRELIMINARY; PRT; 354 AA.
AC Q9MW41
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE MHC class I antigen Mamu-B*12 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96386644; PubMed=8794394;
RA Voss G., Letvin N.L.;
RT "Definition of human immunodeficiency virus type 1 gp120 and gp41
RT cytotoxic T-lymphocyte epitopes and their restricting major
RT histocompatibility complex class I alleles in simian-human
RT immunodeficiency virus-infected rhesus monkeys.";
RL J. Virol. 70:7335-7340 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Voss G., Letvin N.L.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; AF243178; AAF43719.1; -.
DR HSSP; Q95352; 1HKK.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON TER
SQ SEQUENCE 354 AA; 39753 MW; 988448067B84EF23 CRC64;

Query Match 82.7%; Score 1237; DB 7; Length 354;
Best Local Similarity 82.4%; Pred. No. 1.2e-99;
Matches 225; Conservative 15; Mismatches 34; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPFWVEQGPQYW 60
DB 17 GSHSMRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAESPMEPRPFWVEQGPQYW 76

QY 61 EWTGYAKANAQTRVALNRLLRRYNNQSEAGSHLTQMGNGCDMPDGRLLRGYHQAIDG 120
DB 77 EOTRANAKANAQTRVSLGNRLRYNNQSEAGSHLTQMGNGCDMPDGRLLRGYHQAIDG 136
QY 121 KDYISLNEDLSWTAADTVAQITQRFVEAEYAEERFYLEGECLELLRRYLENGKETLQ 180
DB 137 KDYIALNEDLSWTAADTVAQITQRFVEAEYAEERFYLEGECLELLRRYLENGKETLQ 196
QY 181 RADPPKAAHVAHPISDHEATLRCWALGFYPABITLTWQDGEQDTQDTLVELTRPAGDGT 240
DB 197 RADPPKTHVTHPIPSDHEATLRCWALGFYPABITLTWQDGEQDTQDTLVELTRPAGDGT 256
QY 241 FQKWAUVVPSGEQRYTCHVQHEGLPOPLILRW 274
DB 257 FQKWAUVVPSGEQRYTCHVQHEGLPKPLTLRW 290

RESULT 14
Q9MXK1 PRELIMINARY; PRT; 362 AA.
AC Q9MXK1
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE MHC class I antigen.
GN PATR-B.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
EX MEDLINE=20322475; PubMed=10866106;
RA de Groot N.G., Otting N., Arguello R., Watkins D.I., Doxiadis G.G.M.,
RA Madrigal J.A., Bontrop R.E.;
RT "Major histocompatibility complex class I diversity in a West African
RT chimpanzee population: implications for HIV research.";
RL Immunogenetics 51:398-409 (2000).
RN [2]
RP FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
RP IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; AF168410; AAF72791.1; -.
DR HSSP; P03989; 1HSA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40442 MW; 4E1A081945D3A4F3 CRC64;

Query Match 82.7%; Score 1237; DB 7; Length 362;
Best Local Similarity 82.8%; Pred. No. 1.2e-99;
Matches 227; Conservative 15; Mismatches 32; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPFWVEQGPQYW 60
DB 25 GSQSNRYFTANSPRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPFWVEQGPQYW 84
QY 61 EWTGYAKANAQTRVALNRLLRRYNNQSEAGSHLTQMGNGCDMPDGRLLRGYHQAIDG 120
DB 85 DRNTQIGTQATQDRENLRLTLRLRYNNQSEAGSHLTQMGNGCDMPDGRLLRGYHQAIDG 144

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QY 121 KDYISLNEDLSWTAADTVAQITQRFYEAEEVAEFPRTYLEGECLELLRRYLENGKETLQ 180
DB 145 KDYIALNKDLSWTAADTAAITQIKWEAAARVAEQLRAYLEGTCVWLRYLENGKETLQ 204
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOOTDTTELVTETPAGDGT 240
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQDTQDTLVTETPAGDRT 264
QY 241 FOKWAAVVVPSGEGEORYTCHVQHEGLPQPLILRW 274
DB 265 FOKWAAVVVPSGEGEORYTCHVQHEGLPKPLILRW 298

RESULT 15
Q29934
ID Q29934 PRELIMINARY; PRT; 359 AA.
AC Q29934;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE HLA-B protein (Fragment).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86149317; PubMed=3485286;
RA Szots H., Riethmuller G., Weiss E., Meo T.;
RT "Complete sequence of HLA-B*27 cDNA identified through the
RT characterization of structural markers unique to the HLA-A, -B, and -C
RT allelic series.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; M12678; AA59614.1; -
DR HSP; P03989; IHS.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 359 AA; 40042 MW; 65B534A8980E7A88 CRC64;
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Query Match 82.6%; Score 1236; DB 7; Length 359;
Best Local Similarity 82.5%; Pred. No. 1.5e-99;
Matches 226; Conservative 14; Mismatches 34; Indels 0; Gaps 0;

QY 1 GSHSLRFPSTAVSRPGRGEPRYIAVEYVDDTQFLRFSDAIPRMPEPFWQEGPQYW 60
DB 22 GSHSMRYFHTSVSRPGRGEPRFITGVYVDDTLFVRFSDAASPREPRAPWIEQEGPEY 81
QY 61 EWTTCYAKANAQTRVALNRLRRYNQSEAGSHLTQGMNGCDMGDPGRLLRGVHODYD 120
DB 82 DRETQICAKAQTDREDLRLRYNQSEAGSHLTQNMVCGDVGDPGRLLRGVHODYD 141
QY 121 KDYISLNEDLSWTAADTVAQITQRFYEAEEVAEFPRTYLEGECLELLRRYLENGKETLQ 180
DB 142 KDYIALNKDLSWTAADTAAITQIKWEAAARVAEQLRAYLEGTCVWLRYLENGKETLQ 201
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QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOOTDTTELVTETPAGDGT 240
DB 202 RVDPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQDTQDTLVTETPAGDRT 261
QY 241 FOKWAAVVVPSGEGEORYTCHVQHEGLPQPLILRW 274
DB 262 FOKWAAVVVPSGEGEORYTCHVQHEGLPKPLILRW 295

Search completed: June 18, 2004, 19:28:05
Job time : 47 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:31:27 ; Search time 48 Seconds
(without alignments)
1611.540 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRYFSTAVSRPGRGP.....QRYTCHVQHGELPQPLLRW 274

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1163542 segs, 282313646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	274	100.0	274	12 US-09-819-371-5	Sequence 5, Appli
2	274	100.0	362	12 US-10-257-021-82	Sequence 82, Appli
3	274	100.0	442	16 US-10-408-765A-1887	Sequence 1887, Ap
4	241	88.0	271	9 US-09-925-301-1431	Sequence 1431, Ap
5	175	63.9	362	12 US-09-819-371-4	Sequence 4, Appli
6	119	43.4	215	12 US-09-819-371-6	Sequence 6, Appli
7	70	25.5	186	15 US-10-264-049-4063	Sequence 4063, Ap
8	68	24.8	96	14 US-10-029-386-30718	Sequence 30718, A
9	44	16.1	77	14 US-10-029-386-34273	Sequence 34273, A
10	44	16.1	91	14 US-10-029-386-31089	Sequence 31089, A
11	44	16.1	104	9 US-09-925-302-835	Sequence 835, App
12	44	16.1	104	12 US-09-925-302-835	Sequence 835, App
13	40	14.6	78	14 US-10-029-386-30752	Sequence 30752, A
14	40	14.6	371	12 US-10-210-172-156	Sequence 156, App
15	40	14.6	371	15 US-10-085-198-72	Sequence 72, Appli

16	39	14.2	91	9 US-09-864-761-38005	Sequence 38005, A
17	39	14.2	92	12 US-10-380-880-5	Sequence 5, Appli
18	39	14.2	234	12 US-10-380-880-8	Sequence 8, Appli
19	39	14.2	284	15 US-10-104-047-3648	Sequence 3648, Ap
20	39	14.2	326	12 US-10-380-880-7	Sequence 7, Appli
21	39	14.2	379	12 US-10-210-172-160	Sequence 160, App
22	39	14.2	379	15 US-10-093-463-78	Sequence 78, Appli
23	38	13.9	145	9 US-09-810-560-8	Sequence 8, Appli
24	36	13.1	45	14 US-10-029-386-28883	Sequence 28883, A
25	32	11.7	91	9 US-09-864-761-35461	Sequence 35461, A
26	32	11.7	110	9 US-09-796-692-799	Sequence 799, App
27	32	11.7	110	9 US-09-796-692-2139	Sequence 2139, App
28	32	11.7	110	14 US-10-040-862-799	Sequence 799, App
29	32	11.7	110	14 US-10-040-862-2139	Sequence 2139, App
30	32	11.7	110	15 US-10-057-475B-799	Sequence 799, App
31	32	11.7	110	15 US-10-057-475B-2139	Sequence 2139, App
32	32	11.7	110	15 US-10-154-884B-799	Sequence 799, App
33	32	11.7	110	15 US-10-154-884B-2139	Sequence 2139, App
34	32	11.7	196	12 US-10-262-839-48	Sequence 48, Appli
35	32	11.7	198	15 US-10-264-049-3505	Sequence 3505, Ap
36	29	10.6	280	14 US-10-073-300-6	Sequence 6, Appli
37	29	10.6	280	15 US-10-075-257-6	Sequence 6, Appli
38	29	10.6	365	14 US-10-138-888-23	Sequence 23, Appli
39	29	10.6	389	12 US-10-108-511-2	Sequence 2, Appli
40	29	10.6	415	14 US-10-073-300-5	Sequence 5, Appli
41	29	10.6	415	16 US-10-075-257-5	Sequence 5, Appli
42	29	10.6	510	12 US-10-108-511-5	Sequence 5, Appli
43	28	10.2	96	14 US-10-029-386-28377	Sequence 28377, A
44	23	8.4	117	9 US-09-810-560-9	Sequence 9, Appli
45	23	8.4	361	14 US-10-138-888-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1

US-09-819-371-5
; Sequence 5, Application US/09819371
; Publication No. US2004005344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-5

Query Match 100.0%; Score 274; DB 12; Length 274;
Best Local Similarity 100.0%; Pred. No. 3.8e-265;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GSHSLRYFSTAVSRPGRGPRIAYEYVDDTQFLRFDSDAIPRMPEPREPWQEGPQYW	60
Db	1	GSHSLRYFSTAVSRPGRGPRIAYEYVDDTQFLRFDSDAIPRMPEPREPWQEGPQYW	60
Qy	61	EWTTGYAKNAQTQVALNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLRLRGYHOAYDG	120
Db	61	EWTTGYAKNAQTQVALNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLRLRGYHOAYDG	120
Qy	121	KDYISLNDLSRWSAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENGKETLQ	180
Db	121	KDYISLNDLSRWSAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENGKETLQ	180
Qy	181	RADPPKAHVHHPISDHATLRCLWALGYPAAITLTITWQDGEETQDTVELVETRPAGDGT	240
Db	181	RADPPKAHVHHPISDHATLRCLWALGYPAAITLTITWQDGEETQDTVELVETRPAGDGT	240

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 48
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 57
OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 7.00e-24
US-10-029-386-30752

Query Match 14.6%; Score 40; DB 14; Length 78;
Best Local Similarity 100.0%; Pred. No. 7.3e-32;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 TELVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 267
DB 29 TELVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 68

RESULT 14
US-10-210-172-156
Sequence 156, Application US/10210172
Publication No. US20040043928A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieser, Daniel
APPLICANT: Shinkets, Richard
APPLICANT: Zernhusen, Bryan
APPLICANT: Li, Li
APPLICANT: Ji, Weizhen
APPLICANT: Padigaru, Muralidhara
APPLICANT: Casman, Stacie
APPLICANT: Voss, Edward
APPLICANT: Boldog, Ferenc
APPLICANT: Gorman, Linda
APPLICANT: Leite, Mario
APPLICANT: Vernet, Corine
APPLICANT: Anderson, David
APPLICANT: Guo, Xiaojia
APPLICANT: Zhong, Mei
APPLICANT: Gerlach, Valerie
APPLICANT: Hjal, Tor-d
APPLICANT: Rastelli, Luca
APPLICANT: Spytek, Kimberly
APPLICANT: Edinger, Shlomit
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
FILE REFERENCE: 21402-416 A
CURRENT APPLICATION NUMBER: US/10/210,172
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323,994
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,544
PRIOR FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (95)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match 16.1%; Score 44; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 9.6e-36;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 267
DB 32 QTQDTLTVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 75

RESULT 12
US-09-925-302-835
Sequence 835, Application US/09925302
Publication No. US20030064072A9
GENERAL INFORMATION:
APPLICANT: Rozen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 835
LENGTH: 104
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (95)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match 16.1%; Score 44; DB 12; Length 104;
Best Local Similarity 100.0%; Pred. No. 9.6e-36;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 267
DB 32 QTQDTLTVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 75

RESULT 13
US-10-029-386-30752
Sequence 30752, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ACOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 30752
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR6.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.7

; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 327

; SOFTWARE: Curaseqlist version 0.1

; SEQ ID NO 156

; LENGTH: 371

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-210-172-156

Query Match 14.6%; Score 40; DB 12; Length 371;
Best Local Similarity 100.0%; Pred. No. 3e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 TELVETRPAGDGTQKWAADVVPSPGGEORYTCHVQHEGLP 267

Db 250 TELVETRPAGDGTQKWAADVVPSPGGEORYTCHVQHEGLP 289

RESULT 15

US-10-085-198-72

; Sequence 72, Application US/10085198

; Publication No. US20040009907A1

; GENERAL INFORMATION:

; APPLICANT: Alsebrook et al.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-279

; CURRENT APPLICATION NUMBER: US/10/085,198

; CURRENT FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: 60/271,646

; PRIOR FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: 60/276,401

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/311,981

; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: 60/312,858

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 60/271,840

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 60/277,324

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: 60/286,096

; PRIOR FILING DATE: 2001-04-21

; PRIOR APPLICATION NUMBER: 60/299,695

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: 60/315,614

; PRIOR FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/272,405

; PRIOR FILING DATE: 2001-02-28

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 653

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 72

; LENGTH: 371

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-085-198-72

Query Match 14.6%; Score 40; DB 15; Length 371;
Best Local Similarity 100.0%; Pred. No. 3e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 TELVETRPAGDGTQKWAADVVPSPGGEORYTCHVQHEGLP 267

Db 250 TELVETRPAGDGTQKWAADVVPSPGGEORYTCHVQHEGLP 289

Search completed: June 18, 2004, 19:37:21
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:26:06 ; Search time 61 Seconds
(without alignments)
1269.148 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRVFSTAVSRPGRGP.....QRYTCHVQHGGLPOLILRW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	274	4	AAG64618 Human can
2	274	100.0	362	4	AAG64617 Human can
3	274	100.0	362	4	AB50296 HLA-Cw ov
4	250	91.2	677	4	ABG26726 Novel hum
5	241	88.0	271	3	AAB43986 Human can
6	215	78.5	215	4	AAG64619 Human can
7	99	35.1	120	3	AAG00209 Human sec
8	70	25.5	186	5	ABP42931 Human ova
9	44	16.1	104	3	AB58497 Lung canc
10	44	16.1	274	1	ABP80911 Consensus
11	44	16.1	366	2	AAR12466 HLA-C exo
12	44	16.1	366	2	AAY07033 Breast ca
13	44	16.1	374	4	AAC13073 Human pol
14	44	16.1	380	4	AAC13283 Novel hum
15	43	15.7	120	4	AB90793 Human she
16	43	15.7	362	7	AD311177 Human dia
17	40	14.6	371	7	AD40250 Human NOV
18	39	14.2	91	4	AB18379 Peptide #
19	39	14.2	91	4	AB37410 Peptide #
20	39	14.2	91	4	AA30858 Peptide #
21	39	14.2	91	4	AB32163 Peptide #
22	39	14.2	91	4	AB222707 Protein #
23	39	14.2	91	4	AAW70538 Human bon
24	39	14.2	91	4	AA58091 Human bra
25	39	14.2	91	4	AB52217 Human liv

26	39	14.2	91	4	AA05976 Peptide #
27	39	14.2	91	5	ABG40192 Human pep
28	39	14.2	92	5	Aau79452 HLA-G alp
29	39	14.2	234	5	Aau79455 HLA-G rec
30	39	14.2	284	7	ADB5494 Human pro
31	39	14.2	326	5	Aau79454 HLA-G rec
32	39	14.2	338	7	ADD46572 Human pro
33	39	14.2	379	5	ABP70087 Human NOV
34	39	14.2	379	7	ADE40254 Human NOV
35	32	11.7	91	4	AA15751 Peptide #
36	32	11.7	91	4	ABB34748 Peptide #
37	32	11.7	91	4	AA28260 Peptide #
38	32	11.7	91	4	ABB29570 Peptide #
39	32	11.7	91	4	ABB20163 Protein #
40	32	11.7	91	4	AA67933 Human bon
41	32	11.7	91	4	AA55549 Human bra
42	32	11.7	91	4	ABG49576 Human liv
43	32	11.7	91	4	AA03485 Peptide #
44	32	11.7	91	5	ABG37468 Human pep
45	32	11.7	110	4	AA81775 Human hae

ALIGNMENTS

RESULT 1
AAG64618
ID AAG64618 standard; protein; 274 AA.
XX
AC AAG64618;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human cancer cell specific HLA-F antigen SEQ ID 5.
XX
KW HLA-F antigen; cancer cell specific; human.
XX
OS Homo sapiens.
XX
FN JP2001095584-A.
XX
PD 10-APR-2001.
XX
PF 30-SEP-1999; 99JP-00279566.
XX
PR 30-SEP-1999; 99JP-00279566.
XX
PA (EGAW/) EGAWA K.
PA (MEDI-) MEDINET KK.
XX (KIMU/) KIMURA K.
XX
DR WPI; 2001-360493/38.
DR N-PSDB; AAH45556.
XX
PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX
PS Claim 2; Page 10-11; 12pp; Japanese.
XX
CC This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present CC sequence represents the cancer cell-specific HLA-F antigen of the CC invention

Query Match 100.0%; Score 274; DB 4; Length 274;

Best Local Similarity 100.0%; Pred. No. 5.3e-250;

Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRVFSTAVSRPGRGPRIYAVEYDQTFLRPSDAAIPMEPRFWVSGEPQYW 60

Db 1 GSHSLRYSTAVSRGPRGEPRYIAVEYDDTQFLRFDSDAAIPRMEPRPFWVEQGPQYW 60
QY 61 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
Db 61 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
QY 121 KDYISLNEDLSRWSAATVAQITQRFYAEABEYAEFTYLEGCELELLRRYLENGKETLQ 180
Db 121 KDYISLNEDLSRWSAATVAQITQRFYAEABEYAEFTYLEGCELELLRRYLENGKETLQ 180
QY 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGESECTODTELVEVTRPAGDGT 240
Db 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGESECTODTELVEVTRPAGDGT 240
QY 241 FQKWAADVVPSEGEORYTCHVQHEGLPOPLILRW 274
Db 241 FQKWAADVVPSEGEORYTCHVQHEGLPOPLILRW 274
RESULT 2
AAG64617
ID AAG64617 standard; protein; 362 AA.
AC AAG64617;
XX
DT 12-SEP-2001 (first entry)
DE Human cancer cell specific HLA-F antigen SEQ ID 4.
KW HLA-F antigen; cancer cell specific; human.
XX Homo sapiens.
OS
FN JP2001095584-A.
XX
XX 10-APR-2001.
XX
XX 30-SEP-1999; 99JP-00279566.
XX
XX 30-SEP-1999; 99JP-00279566.
XX (EGAW//) EGAWA K.
PA (MEDI-) MEDINET KK.
PA (KIMU//) KIMURA K.
XX
XX WPI; 2001-360493/38.
DR N-PSDB; AAH45555.
XX
XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
PT
PS Disclosure; Page 9-10; 12pp; Japanese.
XX
XX This invention relates to a cancer cell specific HLA-F antigen. The
CC invention includes DNA encoding the antigen, and a method for the
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
CC used in a method to diagnose cancer, in which the protein is used to
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
CC sequence represents the cancer cell-specific HLA-F antigen of the
CC invention
XX
SQ Sequence 362 AA;
Query Match 100.0%; Score 274; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 6.6e-250;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHSLRYSTAVSRGPRGEPRYIAVEYDDTQFLRFDSDAAIPRMEPRPFWVEQGPQYW 60
Db 22 GSHSLRYSTAVSRGPRGEPRYIAVEYDDTQFLRFDSDAAIPRMEPRPFWVEQGPQYW 81
QY 61 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120

Db 82 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141
QY 121 KDYISLNEDLSRWSAATVAQITQRFYAEABEYAEFTYLEGCELELLRRYLENGKETLQ 180
Db 142 KDYISLNEDLSRWSAATVAQITQRFYAEABEYAEFTYLEGCELELLRRYLENGKETLQ 201
QY 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGESECTODTELVEVTRPAGDGT 240
Db 202 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGESECTODTELVEVTRPAGDGT 261
QY 241 FQKWAADVVPSEGEORYTCHVQHEGLPOPLILRW 274
Db 262 FQKWAADVVPSEGEORYTCHVQHEGLPOPLILRW 295
RESULT 3
ABB50296
ID ABB50296 standard; protein; 362 AA.
XX
AC ABB50296;
XX
DT 08-FEB-2002 (first entry)
DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.
XX
XX Ovarian tumour marker gene; human; overexpression; upregulation;
KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
KW identification; serous cystadenoma; borderline serous tumour;
KW serous cystadenocarcinoma; mucinous mucinous tumour; endometrioid carcinoma;
KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
KW immune response pathway; cell proliferation regulation; protein folding;
KW membrane localised; secreted; therapeutic target; cytostatic;
KW gene therapy; vaccine.
XX
XX Homo sapiens.
OS
XX WO200175177-A2.
XX
XX 11-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US010947.
XX
XX 03-APR-2000; 2000US-0194336P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
XX WPI; 2001-626450/72.
DR N-PSDB; ABA83122.
XX
XX Detecting and identifying ovarian tumor, identifying increased risk for
PT developing ovarian cancer, and determining effectiveness of ovarian
PT cancer treatment, by measuring expression level of ovarian tumor marker
PT gene.
XX
XX Claim 23; Page 126-127; 140pp; English.
XX
XX The invention relates to methods for diagnosing and prognosing ovarian
CC tumours in an individual via the detection and measurement of the
CC expression of ovarian tumour marker genes (ABA831081-ABA83122, ABA83180,
CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
CC ABA83181 and ABA83183). The methods of the invention are useful for
CC detecting an ovarian tumour in a patient, for identifying an individual
CC at increased risk for developing ovarian cancer, in prognostic tests for
CC assessing the relative severity of ovarian cancer, in tests for
CC monitoring a patient in remission from ovarian cancer and in tests for
CC monitoring disease status in a patient being treated for ovarian cancer.
CC The methods can additionally be used to identify a particular tumour as
CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,

CC mucinous cystadenoma, borderline mucinous tumour, mucinous
CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
CC tumour. The ovarian tumour marker genes of the invention were identified
CC using SAGE (serial analysis of gene expression) and were found to be
CC overexpressed in a broad variety of ovarian epithelial tumour cells
CC relative to normal ovarian epithelial cells. The marker genes are
CC implicated in immune response pathways, in the regulation of cell
CC proliferation and in protein folding, and many of these are membrane-
CC localised or secreted. In addition to their use as diagnostic and
CC prognostic markers, the ovarian tumour marker genes or their encoded
CC proteins may be used as therapeutic targets for the treatment and
CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent
CC proteins encoded by ovarian tumour marker genes of the invention
XX
SQ Sequence 362 AA;

Query Match 100.0%; Score 274; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 6.6e-250;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAIPRMEPREPWEQGPQYW 60
Db 22 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAIPRMEPREPWEQGPQYW 81

Qy 61 EWTTCYAKANAQTDRAVALNLLRRYNOSEAGSHTLQGMNGCDMGDPDGLRLGYHQHAYDG 120
Db 82 EWTTCYAKANAQTDRAVALNLLRRYNOSEAGSHTLQGMNGCDMGDPDGLRLGYHQHAYDG 141

Qy 121 KDYISLNEEDLSRWSAATVAQITQRFYEABEYAEFFTYLEGECLLELLRRYLENGKETLQ 180
Db 142 KDYISLNEEDLSRWSAATVAQITQRFYEABEYAEFFTYLEGECLLELLRRYLENGKETLQ 201

Qy 161 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVELTRPAGDGT 240
Db 202 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVELTRPAGDGT 261

Qy 241 FQKWAAVVPSGEQRYTCHVQHEGLPQLILRW 274
Db 262 FQKWAAVVPSGEQRYTCHVQHEGLPQLILRW 295

RESULT 4
ABG26726
ID ABG26726 standard; protein; 677 AA.
XX
AC ABG26726;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #26717.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS90913.
XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 57085; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 677 AA;

Query Match 91.2%; Score 250; DB 4; Length 677;
Best Local Similarity 100.0%; Pred. No. 4.7e-227;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAIPRMEPREPWEQGPQYW 60
Db 331 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAIPRMEPREPWEQGPQYW 390

Qy 61 EWTTCYAKANAQTDRAVALNLLRRYNOSEAGSHTLQGMNGCDMGDPDGLRLGYHQHAYDG 120
Db 391 EWTTCYAKANAQTDRAVALNLLRRYNOSEAGSHTLQGMNGCDMGDPDGLRLGYHQHAYDG 450

Qy 121 KDYISLNEEDLSRWSAATVAQITQRFYEABEYAEFFTYLEGECLLELLRRYLENGKETLQ 180
Db 451 KDYISLNEEDLSRWSAATVAQITQRFYEABEYAEFFTYLEGECLLELLRRYLENGKETLQ 510

Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVELTRPAGDGT 240
Db 511 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVELTRPAGDGT 570

Qy 241 FQKWAAVVVP 250
Db 571 FQKWAAVVVP 580

RESULT 5
AAB43986
ID AAB43986 standard; protein; 271 AA.
XX
AC AAB43986;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated protein sequence SEQ ID NO:1431.
XX
KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW disnoeais; cytostatic; proliferative; vulnery; immunomodulator;
KW antidiabetic; antistatic; antirheumatic; antiarthritic; antiviral;
KW antinflammatory; antichryoid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
XX

KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.

OS Homo sapiens.
XX WO20005350-A1.
XX 21-SEP-2000.
XX 08-MAR-2000; 2000WO-US005882.
XX 12-MAR-1999; 99US-0124270P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2000-587533/55.
XX N-PSDB; AAC78195.

Novel isolated nucleic acids comprising sequences encoding peptides
useful for treating or diagnosing e.g. cancer.

Claim 11; Page 2115-2116; 2352pp; English.

AAC77607 to AAC78448 encode the human cancer associated proteins given in
AAB43398 to AAB44239. The proteins can have activities based on the
tissues and cells the genes are expressed in. Example of activities
include: cytostatic; proliferative; vulnery; immunomodulator;
CC anti-diabetic; antiasthmatic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC neotropic; vasotropic; antiporiatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention

Sequence 271 AA;

Query Match 88.0%; Score 241; DB 3; Length 271;
Best Local Similarity 100.0%; Pred. No. 7.1e-219;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHSLRSTAVSRPGRGEPIYIAVEYVDDTQFLRFSDAAIPRMEPREPWVEGPGQYW 60
Db 28 GSHSLRSTAVSRPGRGEPIYIAVEYVDDTQFLRFSDAAIPRMEPREPWVEGPGQYW 87
QY 61 EMTTGYAKANAQTDVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDG 120
Db 88 EMTTGYAKANAQTDVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDG 147
QY 121 KDYISLNEDLSRWSAADTAQITQRFYEAEBYAEFRFYLEGECLELLRRYLENGKETLQ 180
Db 148 KDYISLNEDLSRWSAADTAQITQRFYEAEBYAEFRFYLEGECLELLRRYLENGKETLQ 207
QY 161 RADPPKAHVHPIPSDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVETRPAGDT 240
Db 208 RADPPKAHVHPIPSDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVETRPAGDT 267
QY 241 F 241
Db 268 F 263

RESULT 6
AAG64619

ID AAG64619 standard; protein; 215 AA.

XX AAG64619;

AC AAG64619;

XX 12-SEP-2001 (first entry)

XX Human cancer cell specific HLA-F antigen SEQ ID 6.

XX HLA-F antigen; cancer cell specific; human.

OS Homo sapiens.

XX JP2001095584-A.

XX 10-APR-2001.

XX 30-SEP-1999; 99JP-00279566.

XX 30-SEP-1999; 99JP-00279566.

XX (EGAW/) EGAWA K.

XX (MEDI-) MEDINET KK.

XX (KIMU/) KIMURA K.

XX WPI; 2001-360493/38.

XX N-PSDB; AAH45557.

XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.

XX Claim 1; Page 11-12; 12pp; Japanese.

XX This invention relates to a cancer cell specific HLA-F antigen. The
invention includes DNA encoding the antigen, and a method for the
preparation of the cancer cell specific HLA-F antigen. The antigen may be
used in a method to diagnose cancer, in which the protein is used to
detect anti-HLA-F antibodies in bodily fluids of the patient. The present
sequence represents the cancer cell-specific HLA-F antigen of the
invention

XX Sequence 215 AA;

Query Match 78.5%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 2e-194;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEGPGQYWEWTTGYAKANAQTDVALRNLL 82

Db 1 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEGPGQYWEWTTGYAKANAQTDVALRNLL 60

QY 83 RRYNQEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDGKDYISLNEDLSRWSAADTAQI 142

Db 61 RRYNQEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDGKDYISLNEDLSRWSAADTAQI 120

QY 143 TQRFYEAEBYAEFRFYLEGECLELLRRYLENGKETLQADPPKAHVHPIPSDHEATLR 202

Db 121 TQRFYEAEBYAEFRFYLEGECLELLRRYLENGKETLQADPPKAHVHPIPSDHEATLR 180

QY 203 CWALGFYPAEITLTWQDGEEOQTDELVETRPAG 237

Db 181 CWALGFYPAEITLTWQDGEEOQTDELVETRPAG 215

RESULT 7

XX AAG00209

ID AAG00209 standard; protein; 120 AA.

XX AAG00209;

XX 06-OCT-2000 (first entry)

```
XX Human secreted protein, SEQ ID NO: 4290.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX Gene therapy; chromosome mapping.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX N-PSDB; AAC00215.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 13; SEQ ID NO 4290; 71pp - Sequence Listing; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number of
XX 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX tissues. EST sequences usually correspond mainly to the 3' untranslated
XX region (UTR) of the mRNA because they are often obtained from oligo-dT
XX primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX sequences derived from the 5' ends of mRNAs and even in those cases where
XX longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX are also used in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures. They are used to obtain upstream regulatory sequences
XX and to design expression and secretion vectors
XX
XX Sequence 120 AA;
XX
XX Query Match 36.1%; Score 99; DB 3; Length 120;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-85;
XX Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GSHSLYFSTAVSRPGRGEPRIYAVYVDVTQFLRFDSDAALPRMEPRPWEQEGPQYW 60
XX DB 22 GSHSLYFSTAVSRPGRGEPRIYAVYVDVTQFLRFDSDAALPRMEPRPWEQEGPQYW 81
XX
XX QY 61 EMTTGYAKANAQTDRLVALNLLRRYNSQAGSHTLQGMN 99
XX DB 82 EMTTGYAKANAQTDRLVALNLLRRYNSQAGSHTLQGMN 120
XX
XX RESULT 8
XX ABP42931
XX ID -ABP42931 standard; protein; 186 AA.
XX
XX AC ABP42931;
XX
XX XX 22-AUG-2002 (first entry)
XX
XX Human ovarian antigen HPDRT37, SEQ ID NO:4063.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
XX inflammatory condition; immune disorder; blood disorder;
```

```
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
XX OS Homo sapiens.
XX
XX WO200200677-A1.
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US018569.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-147878/19.
XX
XX N-PSDB; ABQ56008.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX cancer), immune disorders, cardiovascular disorders and neurological
XX diseases.
XX
XX Claim 11; SEQ ID NO 4063; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX respiratory disorders, neurological disorders, gastrointestinal disorders
XX and urinary system disorders. Ovarian antigen polypeptides and
XX polynucleotides may also be used in screening for compounds which
XX modulate ovarian antigen expression or activity. The polynucleotides may
XX further be used for gene therapy, chromosome mapping, in the
XX identification of individuals and in forensic analysis, and the
XX polypeptides may be used as food additives or to prepare antibodies
XX useful in disease diagnosis, drug targeting and phenotyping. The present
XX sequence represents a human ovarian antigen of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 186 AA;
XX
XX Query Match 25.5%; Score 70; DB 5; Length 186;
XX Best Local Similarity 100.0%; Pred. No. 1e-57;
XX Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 66 YAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNCGDMPDGRLLRGYHQAIDGKDYIS 125
XX DB 1 YAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNCGDMPDGRLLRGYHQAIDGKDYIS 60
XX
XX QY 126 LNEDLRSWTA 135
XX DB 61 LNEDLRSWTA 70
```

AAAP80911 standard; protein; 274 AA.
AAP80911;
25-MAR-2003 (revised)
18-SEP-1990 (first entry)
Consensus sequence of peptides which constitute the alpha-1, alpha-2 and alpha-3 regions of a class I HLA molecule.
HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3.
Homo sapiens.
Key Location/Qualifiers
Region 1..90 /note= "alpha-1 region"
Region 91..180 /note= "alpha-2 region"
Region 181..272 /note= "alpha-3 region"
WO805784-A.
11-AUG-1988.
27-JAN-1988; 88WO-US000245.
30-JAN-1987; 87US-0008846.
24-DEC-1987; 87US-00138547.
(STRD) UNIV LELAND STANFORD JUNIOR.
Krensky AM, Farham P, Clayberger C;
WPI; 1988-235147/33.
New peptide corresp. to major histocompatibility antigen regions - used for modulating cytotoxic T-lymphocyte activity in e.g. transplants or auto-immune diseases.
Example 9; Fig 4; 60pp; English.
The consensus sequence is derived from a total of 23 HLA-A,B,C sequences. The protein sequences in the three extracellular domains (alpha-1, alpha-2 and alpha-3) are shown. The example concerned the effect of peptides from different HLA-A2 epitopes on cytotoxicity of target cells by CTL of different specificities. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
Sequence 274 AA;
Query Match 16.1%; Score 44; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 4.8e-33;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 QTQDTLTVETRPAGDGTFOKMAAVVPSGEEQRYTCHVQHEGLP 267
DB 224 QTQDTLTVETRPAGDGTFOKMAAVVPSGEEQRYTCHVQHEGLP 267
RESULT 11
AAR12466
ID AAR12466 standard; protein; 366 AA.
XX AAR12466;
AC AAR12466;
XX 25-MAR-2003 (revised)
DT 29-AUG-1991 (first entry)
XX HLA-C exon Cb-2.
XX

AAAB58497 standard; protein; 104 AA.
AAB58497;
14-MAR-2001 (first entry)
Lung cancer associated polypeptide sequence SEQ ID 835.
Human; lung cancer associated protein; neuroprotective; cytosolic; cardiolipase; immunomodulatory; muscular active; vulnery; gastrointestinal; nephrotropic; antineoplastic; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
Homo sapiens.
WO2000055180-A2.
21-SEP-2000.
08-MAR-2000; 2000WO-US005918.
12-MAR-1999; 99US-0124270P.
(HUMA-) HUMAN GENOME SCI INC.
(ROSE/) ROSEN C A.
Ruben SM;
WPI; 2000-587514/55.
N-PSDB; AAF18373.
Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer.
Claim 11; Page 1375; 1425pp; English.
Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytosolic; cardiolipase; immunomodulatory; muscular active general; vulnery; gastrointestinal general; nephrotropic; antineoplastic; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein sequences
Sequence 104 AA;
Query Match 16.1%; Score 44; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.2e-33;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 QTQDTLTVETRPAGDGTFOKMAAVVPSGEEQRYTCHVQHEGLP 267
DB 32 QTQDTLTVETRPAGDGTFOKMAAVVPSGEEQRYTCHVQHEGLP 75
RESULT 10
AAP80911

KW Human leukocyte antigen; probe; major histocompatibility complex; MHC;
KW class I.
XX Homo sapiens.
OS JP03112485-A.
PN 14-MAY-1991.
PD 22-SEP-1989; 89JP-00247695.
XX 22-SEP-1989; 89JP-00247695.
XX (OLYU) OLYMPUS OPTICAL CO LTD.
PA WPI; 1991-182989/25.
DR N-PSDB; AAQ12117.
XX HLA-C gene, DNA probe and transformant cells - for immunisation of
PT animals and monoclonal antibody development.
XX Claim 4; Page 2; 13pp; Japanese.
XX Probes comprising part of the DNA sequence encoding the protein can be
CC used to identify Class I genes. The DNA can be expressed for immunisation
CC of animals and prodn. of monoclonal antibodies specific for the HLA-C
CC antigen. See also AAP12465 (same patent) and J03112486 and J03112487.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 366 AA;
Query Match 16.1%; Score 44; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 6e-33;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 QTQDTLVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267
Db 248 QTQDTLVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 291
RESULT 12
AAQ07033
ID AAY07033 standard; protein; 366 AA.
AC AAY07033;
XX 02-JUL-1999 (first entry)
DE Breast cancer associated antigen precursor sequence.
XX Cancer associated antigen; diagnosis; research; treatment; human;
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW prostate cancer.
XX Homo sapiens.
OS WO9904265-A2.
XX 28-JAN-1999.
XX 15-JUL-1998; 98WO-US014679.
XX 17-JUL-1997; 97US-00896164.
PR 10-OCT-1997; 97US-00611599P.
PR 10-OCT-1997; 97US-0061765P.
PR 10-OCT-1997; 97US-00948705.
PR 11-OCT-1997; 97GB-00021697.
PR 22-JUN-1998; 98US-0010322.
XX (LUDW-) LUDWIG INST CANCER RES.
PA Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
XX O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;

XX WPI; 1999-132448/11.
DR New isolated cancer associated nucleic acids and polypeptides - isolated
XX using sera from cancer patients, used to develop products for the
PT diagnosis, monitoring or treatment of cancers.
XX Disclosure; Page 417-418; 787pp; English.
XX The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
CC binds to the NAM, an expression product or a fragment of an expression
CC product complexed with an HLA molecule; and (b) determining the
CC interaction between the agent and the NAM or the expression product as a
CC determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
CC characterised by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC which are cancer associated antigen precursors expressed in human breast
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC lung cancer
XX SQ Sequence 366 AA;
Query Match 16.1%; Score 44; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 6e-33;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 QTQDTLVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267
Db 248 QTQDTLVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 291
RESULT 13
AAQ13073
ID AAQ13073 standard; protein; 374 AA.
XX AAQ13073;
XX 06-NOV-2001 (first entry)
XX Human polypeptide SEQ ID NO 26965.
DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX Homo sapiens.
OS WO200164835-A2.
XX 07-SEP-2001.
XX 26-FEB-2001; 2001WO-US004927.
XX 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
PI WPI; 2001-514838/56.
XX N-PSDB; AA193004.
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX Claim 20; SEQ ID NO 26965; 1399pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI79941-AA193841) and the encoded proteins (AAO00010-AAO1910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match	16.1%	Score 44	DB 4	Length 374
Best Local Similarity	100.0%	Fred.NC. 6.1e-33		
Matches 44	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	224	QTQTELVETRPAGDGFQKAAAVVPSGGEQRVYTCVQHEGLP	267
Db	256	QTQTELVETRPAGDGFQKAAAVVPSGGEQRVYTCVQHEGLP	299

RESULT 14	
AAU32883	
ID	AAU32883 standard; protein; 380 AA.
XX	
XX	
XX	AAU32883;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Novel human secreted protein #3374.
XX	
XX	Human; vaccination; gene therapy; nutritional supplement;
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX	Homo sapiens.
OS	
XX	WO200179449-A2.
PN	
XX	25-OCT-2001.
PD	
XX	16-APR-2001; 2001WO-US008656.
PF	
XX	18-APR-2000; 2000US-00552929.
PR	
XX	26-JAN-2001; 2001US-00770160.
XX	(HYSE-) HYSEQ INC.
PA	
XX	Tang YT, Liu C, Drmanac RT;
PI	
XX	WPI; 2001-611735/70.
DR	
XX	Nucleic acids encoding a range of human polypeptides, useful in genetic
PT	vaccination, testing and therapy.
PS	Claim 20; Page 683-684; 765pp; English.

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell

CC proliferation; to regulate haematopoiesis; and in bone cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU3304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
XX
SO Sequence 380 AA;
SO

Query Match	16.1%	Score 44;	DB 4;	Length 380;
Best Local Similarity	100.0%	Pred. No. 6.2e-33;		
Matches 44;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	224	QTQDTLVETRPAGDGTQKAAVVVPSGEEQRYTCHVQHEGLP	267
Db	256	QTQDTLVETRPAGDGTQKAAVVVPSGEEQRYTCHVQHEGLP	299

RESULT 15
AAB90793
ID AAB90793 standard; protein; 120 AA.
XX
XX AAB90793;
XX AC
XX AC
DT 15-JUN-2001 (first entry)

DE	Human shear stress-response protein SEQ ID NO: 86.
XX	
XX	Human; shear stress-response protein; vascular disease; arteriosclerosis.
KW	
XX	
XX	
OS	Homo sapiens.
XX	
XX	WO200125427-A1.
PN	
XX	
XX	12-APR-2001.
XX	
XX	02-OCT-2000; 2000WO-JP006840.
PF	
XX	
XX	01-OCT-1999; 99JP-00280976.
PR	
XX	
XX	(KYOW) KYOWA HAKKO KOGYO KK.
PA	(NOJI/) NOUIMA H.
PA	
XX	
XX	Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI	Kuga T, Sekine S, Nakamura Y, Sugano S;
PI	WPI; 2001-366308/27.
XX	N-PSDB; AAH02916.
DR	
DR	

XX DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis.
XX
PS Claim 60; Page 471-472; 678pp; Japanese.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PICA stenosis and
CC hypertension

```

SQ      Sequence 120 AA;

Query Match      15.7%;      Score 43;      DB 4;      Length 120;
Best Local Similarity 100.0%;      Pred. No. 2.2e-32;
Matches 43;      Conservative 0;      Mismatches 0;      Indels 0;      Gaps 0

Qy      225      TQTELVETRRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267
Db      8      TQTELVETRRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 50

```

Search completed: June 18, 2004, 19:29:54
Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:27:12 ; Search time 45 Seconds
(without alignments)
1921.155 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRYSTAVSRGRGEP.....QRYTCHVQHEGLPQLILRW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL 25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriaph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	324	7 Q861F0	Q861F0 homo sapien
2	274	100.0	324	7 Q861E9	Q861E9 homo sapien
3	274	100.0	346	7 Q8WLP5	Q8WLP5 homo sapien
4	274	100.0	442	7 Q95HC0	Q95HC0 homo sapien
5	250	91.2	346	7 Q8MGQ1	Q8MGQ1 homo sapien
6	250	91.2	362	7 Q9TP68	Q9TP68 homo sapien
7	208	75.9	346	7 Q95IT2	Q95IT2 pan troglod
8	208	75.9	362	7 Q7YR27	Q7YR27 pan troglod
9	182	66.4	254	7 Q860R0	Q860R0 homo sapien
10	87	31.8	91	7 Q9TXX7	Q9TXX7 Sorilla gor
11	73	26.6	316	7 Q29958	Q29958 homo sapien
12	62	22.6	314	7 Q860F6	Q860F6 macaca neme
13	61	22.3	353	7 Q9MXS7	Q9MXS7 macaca mula
14	61	22.3	353	7 Q9MXS6	Q9MXS6 macaca mula
15	61	22.3	365	7 Q9MXS5	Q9MXS5 macaca mula
16	59	21.5	59	7 Q78094	Q78094 homo sapien

17	45	16.4	330	7	Q30713	Q30713 macaca mula
18	45	16.4	338	7	Q95510	Q95510 leopardus p
19	45	16.4	359	7	Q30711	Q30711 macaca mula
20	44	16.1	91	7	Q9MY12	Q9MY12 homo sapien
21	44	16.1	91	7	Q9MY10	Q9MY10 homo sapien
22	44	16.1	91	7	Q9MYH8	Q9MYH8 homo sapien
23	44	16.1	91	7	Q7YP25	Q7YP25 homo sapien
24	44	16.1	91	7	Q7YNY6	Q7YNY6 homo sapien
25	44	16.1	91	7	Q7YNY3	Q7YNY3 homo sapien
26	44	16.1	259	7	Q29645	Q29645 homo sapien
27	44	16.1	273	7	Q9GIP0	Q9GIP0 homo sapien
28	44	16.1	273	7	Q9BCN8	Q9BCN8 homo sapien
29	44	16.1	273	7	Q8SNC6	Q8SNC6 homo sapien
30	44	16.1	273	7	Q8MGZ8	Q8MGZ8 homo sapien
31	44	16.1	273	7	Q9TQP8	Q9TQP8 homo sapien
32	44	16.1	273	7	Q8HWT0	Q8HWT0 homo sapien
33	44	16.1	273	7	Q95IG6	Q95IG6 homo sapien
34	44	16.1	298	7	Q29866	Q29866 homo sapien
35	44	16.1	298	7	P79497	P79497 homo sapien
36	44	16.1	298	7	O19657	O19657 homo sapien
37	44	16.1	298	7	O19653	O19653 homo sapien
38	44	16.1	298	7	O19655	O19655 homo sapien
39	44	16.1	312	7	Q860B5	Q860B5 homo sapien
40	44	16.1	312	7	Q860B4	Q860B4 homo sapien
41	44	16.1	313	7	Q30989	Q30989 pan troglod
42	44	16.1	313	7	Q9MY41	Q9MY41 homo sapien
43	44	16.1	314	7	Q860G9	Q860G9 macaca neme
44	44	16.1	318	7	Q7YPW4	Q7YPW4 homo sapien
45	44	16.1	319	7	Q861B7	Q861B7 homo sapien

ALIGNMENTS

RESULT 1

Q861F0 PRELIMINARY; PRT; 324 AA.
ID Q861F0
AC Q861F0; 24, Created
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Nonclassical MHC class I antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Liu Y., Zeng Y.;
RT "Nonclassical MHC class I HLA-F";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY216682; AAO37689.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR PRINTS: PR01638; MHCCLASSI.
DR PRODOM: PD000050; MHC_I; 1.
DR SMART: SM00407; Igc1; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR PROSITE: PS00290; IG_MHC; 1.
FT NON TER 1 324
FT NON TER 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Query Match 100.0%; Score 274; DB 7; Length 324;

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Best Local Similarity 100.0%; Pred. No. 3.1e-279; Indels 0; Gaps 0;
Matches 274; Conservative 0; Mismatches 0;

QY 1 GSHSLRYSTAVSRGGRGPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 60
Db 18 GSHSLRYSTAVSRGGRGPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 77
QY 61 EWTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
Db 78 EWTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 137
QY 121 KDYISLNEDLRSWTAADTVAQITQRFYEAEYAEAEFRVTEGECLELLRRVLENGKETLQ 180
Db 138 KDYISLNEDLRSWTAADTVAQITQRFYEAEYAEAEFRVTEGECLELLRRVLENGKETLQ 197
QY 181 RADPPKARVAHHPISDHEATLRCAWALGFYPAEITLTWQDGEEOQTDTLVEVTRPAGDGT 240
Db 198 RADPPKARVAHHPISDHEATLRCAWALGFYPAEITLTWQDGEEOQTDTLVEVTRPAGDGT 257
QY 241 FQKWAAVVPSGEGQRYTCHVQHEGLPQPLILRW 274
Db 258 FQKWAAVVPSGEGQRYTCHVQHEGLPQPLILRW 291

RESULT 2
Q86LE9 PRELIMINARY; PRT; 324 AA.
ID Q86LE9 AC Q86LE9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Xu L., Zeng Y., He X.;
RT "A new polymorphism in non-classical MHC class I HLA-F.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY221102; AAO34407.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.C1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00129; MHC_I_1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I_1.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1 324
FT NON_TER 324 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Query Match 100.0%; Score 274; DB 7; Length 324;
Best Local Similarity 100.0%; Pred. No. 3.1e-279;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRGGRGPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 60
Db 18 GSHSLRYSTAVSRGGRGPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 77
QY 61 EWTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
Db 78 EWTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 137
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QY 121 KDYISLNEDLRSWTAADTVAQITQRFYEAEYAEAEFRVTEGECLELLRRVLENGKETLQ 180
Db 138 KDYISLNEDLRSWTAADTVAQITQRFYEAEYAEAEFRVTEGECLELLRRVLENGKETLQ 197
QY 181 RADPPKARVAHHPISDHEATLRCAWALGFYPAEITLTWQDGEEOQTDTLVEVTRPAGDGT 240
Db 198 RADPPKARVAHHPISDHEATLRCAWALGFYPAEITLTWQDGEEOQTDTLVEVTRPAGDGT 257
QY 241 FQKWAAVVPSGEGQRYTCHVQHEGLPQPLILRW 274
Db 258 FQKWAAVVPSGEGQRYTCHVQHEGLPQPLILRW 291

RESULT 3
Q8WLP5 PRELIMINARY; PRT; 346 AA.
ID Q8WLP5 AC Q8WLP5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class Ib antigen.
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation spanning the nonclassical class I genes.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA He X., Liu Y., Xu L., Zeng Y.;
RT "Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Liu Y., Zeng Y.;
RT "Cloning of full-length HLA-F*0101 variant 2 cDNA from Han Chinese.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF523285; AAM74980.1; -
DR EMBL; AF523285; AAM74981.1; -
DR EMBL; AF523287; AAM74982.1; -
DR EMBL; AF523288; AAM74983.1; -
DR EMBL; AF523289; AAM74984.1; -
DR EMBL; AF523290; AAM74985.1; -
DR EMBL; AF523293; AAM74988.1; -
DR EMBL; AF523294; AAM74989.1; -
DR EMBL; AF523295; AAM74990.1; -
DR EMBL; AF523296; AAM74991.1; -
DR EMBL; AF523297; AAM74992.1; -
DR EMBL; AY253269; AAO86773.1; -
DR EMBL; AY253270; AAO86774.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00129; MHC_I_1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 100.0%; Score 274; DB 7; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.3e-279;
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Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRPGRGPRYIAVEYDDTQFLRFDSDAAI PRMEPREPWEQGPQYW 60
DB 22 GSHSLRYSTAVSRPGRGPRYIAVEYDDTQFLRFDSDAAI PRMEPREPWEQGPQYW 81
QY 61 EWTGTGAKANAQTDVALNLLRRYNSQAGSHTLQGMNGCDMGPDPGRLLRGYHQHAYDG 120
DB 82 EWTGTGAKANAQTDVALNLLRRYNSQAGSHTLQGMNGCDMGPDPGRLLRGYHQHAYDG 141
QY 121 KYIISLNEDLSRWSWAADTAQITQRFYEAEBEFTYLEGECLELLRRYLENGKETLQ 180
DB 142 KYIISLNEDLSRWSWAADTAQITQRFYEAEBEFTYLEGECLELLRRYLENGKETLQ 201
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTDELVELTRPAGDGT 240
DB 202 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTDELVELTRPAGDGT 261
QY 241 FOKWAAVVVPSGEGORYTCHVQHEGLPQPLILRW 274
DB 262 FOKWAAVVVPSGEGORYTCHVQHEGLPQPLILRW 295

RESULT 4
Q95HCO PRELIMINARY; PRT; 442 AA.
ID Q95HCO
AC Q95HCO;
DT 01-DSC-2001 (T-EMBLrel. 19, Created)
DT 01-DSC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Similar to major histocompatibility complex, class I, P.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009260; AAH09260.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00129; MHC_I.
DR PRINTS; PR01638; MHCCLASSI.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 442 AA; 50427 MW; 6459D3B5F4B5704A CRC64;

Query Match 100.0%; Score 274; DB 7; Length 442;
Best Local Similarity 100.0%; Pred. No. 4.1e-279;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRPGRGPRYIAVEYDDTQFLRFDSDAAI PRMEPREPWEQGPQYW 60
DB 22 GSHSLRYSTAVSRPGRGPRYIAVEYDDTQFLRFDSDAAI PRMEPREPWEQGPQYW 81
QY 61 EWTGTGAKANAQTDVALNLLRRYNSQAGSHTLQGMNGCDMGPDPGRLLRGYHQHAYDG 120
DB 82 EWTGTGAKANAQTDVALNLLRRYNSQAGSHTLQGMNGCDMGPDPGRLLRGYHQHAYDG 141
QY 121 KYIISLNEDLSRWSWAADTAQITQRFYEAEBEFTYLEGECLELLRRYLENGKETLQ 180
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DB 142 KYIISLNEDLSRWSWAADTAQITQRFYEAEBEFTYLEGECLELLRRYLENGKETLQ 201
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTDELVELTRPAGDGT 240
DB 202 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTDELVELTRPAGDGT 261
QY 241 FOKWAAVVVPSGEGORYTCHVQHEGLPQPLILRW 274
DB 262 FOKWAAVVVPSGEGORYTCHVQHEGLPQPLILRW 295

RESULT 5
Q9MGQ1 PRELIMINARY; PRT; 346 AA.
ID Q9MGQ1
AC Q9MGQ1;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE MHC class Ib antigen.
DE HLA-F.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation spanning the nonclassical class I genes.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
CC -! SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AF523284; AAM74979.1; -.
DR EMBL; AF523291; AAM74986.1; -.
DR EMBL; AF523292; AAM74987.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00129; MHC_I.
DR PRINTS; PR01638; MHCCLASSI.
DR PROSITE; PS00050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 346 AA; 39061 MW; D4782968A6759B7D CRC64;

Query Match 91.2%; Score 250; DB 7; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.6e-254;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRPGRGPRYIAVEYDDTQFLRFDSDAAI PRMEPREPWEQGPQYW 60
DB 22 GSHSLRYSTAVSRPGRGPRYIAVEYDDTQFLRFDSDAAI PRMEPREPWEQGPQYW 81
QY 61 EWTGTGAKANAQTDVALNLLRRYNSQAGSHTLQGMNGCDMGPDPGRLLRGYHQHAYDG 120
DB 82 EWTGTGAKANAQTDVALNLLRRYNSQAGSHTLQGMNGCDMGPDPGRLLRGYHQHAYDG 141
QY 121 KYIISLNEDLSRWSWAADTAQITQRFYEAEBEFTYLEGECLELLRRYLENGKETLQ 180
DB 142 KYIISLNEDLSRWSWAADTAQITQRFYEAEBEFTYLEGECLELLRRYLENGKETLQ 201
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTDELVELTRPAGDGT 240
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Db 202 RADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 261
Qy 241 FQKAAVVVP 250
Db 262 FQKAAVVVP 271

RESULT 6
Q9TP68 PRELIMINARY; PRT; 362 AA.
AC Q9TP68 2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE DJ37H14.9 (Major histocompatibility complex, class I, F
  (CDA12)).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AL022723; CAB46623.1; -.
DR HSSP; Q30201; 146Z.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Glycoprotein; Transmembrane.
KW SEQUENCE 362 AA; 40578 MW; 970D072C813A07E2 CRC64;
SQ SEQUENCE 362 AA; 40578 MW; 970D072C813A07E2 CRC64;

Query Match 91.2%; Score 250; DB 7; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.9e-254;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSHSLRYSTAVSRPGRGEPRYIAVEYVDDTQFLRFSDAAIPRMEPRPWPVEQGPQYW 60
Db 22 GSHSLRYSTAVSRPGRGEPRYIAVEYVDDTQFLRFSDAAIPRMEPRPWPVEQGPQYW 81
Qy 61 EWTGYAKANAQTDRLVALNRLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQAHDG 120
Db 82 EWTGYAKANAQTDRLVALNRLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQAHDG 141
Qy 121 KYISLNEDLSRSTAADTVAQITQRFYAEYAEFEFRYLSGECELELLRRYLENGKETLQ 180
Db 142 KYISLNEDLSRSTAADTVAQITQRFYAEYAEFEFRYLSGECELELLRRYLENGKETLQ 201
Qy 181 RADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 240
Db 202 RADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 261
Qy 241 FQKAAVVVP 250
Db 262 FQKAAVVVP 271

RESULT 7
Q95IT2 PRELIMINARY; PRT; 346 AA.
AC Q95IT2 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE MHC class I antigen.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21291697; PubMed=11398964;
RA Adams E.J.; Parham P.;
RT "Genomic analysis of common chimpanzee major histocompatibility
  complex class I genes.";
RL Immunogenetics 53:200-208 (2001).
DR EMBL; AF338355; AAK77479.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;

Query Match 75.9%; Score 208; DB 7; Length 346;
Best Local Similarity 100.0%; Pred. No. 8.1e-210;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 TTGYAKANAQTDRLVALNRLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQAHDG 122
Db 84 TTGYAKANAQTDRLVALNRLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHQAHDG 143
Qy 123 YISLNEDLSRSTAADTVAQITQRFYAEYAEFEFRYLSGECELELLRRYLENGKETLQ 182
Db 144 YISLNEDLSRSTAADTVAQITQRFYAEYAEFEFRYLSGECELELLRRYLENGKETLQ 203
Qy 183 DPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 242
Db 204 DPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 263
Qy 243 KAAAVVVPSEGEQRYTCHVQHEGLPQL 270
Db 264 KAAAVVVPSEGEQRYTCHVQHEGLPQL 291

RESULT 8
Q7YR27 PRELIMINARY; PRT; 362 AA.
AC Q7YR27 2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Class IB.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22709134; PubMed=12799463;
RA Anzai T., Shima T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA Yamagata T., Kuleki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT "Comparative sequencing of human and chimpanzee MHC class I regions
RT unveils insertions/deletions as the major path to genomic
RT divergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
SQ EMBL; AB100087; BAC78191.1; -.
SQ SEQUENCE 362 AA; 40625 MW; BAS699D08181A1FF CRC64;

Query Match 75.9%; Score 208; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 8.5e-210; Indels 0; Gaps 0;
Matches 208; Conservative 0; Mismatches 0;

QY 63 TTGYAKANAQTDVLRNLLRRYNSGASHYLOGMNGCDMPDGRLLRGYHQHAYDGD 122
DB 84 TTGYAKANAQTDVLRNLLRRYNSGASHYLOGMNGCDMPDGRLLRGYHQHAYDGD 143
QY 123 YTSINEDLSRSTAAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENGKETLQRA 182
DB 144 YTSINEDLSRSTAAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENGKETLQRA 203
QY 183 DPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGTQF 242
DB 204 DPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGTQF 263
QY 243 KWAAVVPSGEEQRYTCHVQHEGLPQPL 270
DB 264 KWAAVVPSGEEQRYTCHVQHEGLPQPL 291

RESULT 9
Q860R0 PRELIMINARY; PRT; 254 AA.
ID Q860R0
AC Q860R0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class Ib antigen.
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Liu Y., He X., Xu L., Zeng Y.;
RT "Cloning of full-length HLA-F*0101 variant 3 cDNA from Han Chinese.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY253271; AAC06775.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; C:crystallin.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I.1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
SQ SEQUENCE 254 AA; 28588 MW; C61P225D409AAED2 CRC64;

Query Match 66.4%; Score 182; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-182; Indels 0; Gaps 0;
Matches 182; Conservative 0; Mismatches 0;

QY 1 GSHSLRIFSTAVSPGEGEPRYIAVEYVDTQFLRFDSDAAIPRMEPRPWPVQEGPQYW 60
DB 22 GSHSLRIFSTAVSPGEGEPRYIAVEYVDTQFLRFDSDAAIPRMEPRPWPVQEGPQYW 81
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QY 61 EWTGYAKANAQTDVLRNLLRRYNSGASHYLOGMNGCDMPDGRLLRGYHQHAYDGD 120
DB 82 EWTGYAKANAQTDVLRNLLRRYNSGASHYLOGMNGCDMPDGRLLRGYHQHAYDGD 141
QY 121 KDVISINEDLSRSTAAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENGKETLQ 180
DB 142 KDVISINEDLSRSTAAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENGKETLQ 201
QY 181 RA 182
DB 202 RA 203

RESULT 10
Q9TPX7 PRELIMINARY; PRT; 91 AA.
ID Q9TPX7
AC Q9TPX7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN GOGO-F.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
CX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Shamba;
RA Grimsley C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159566; AAD51614.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0407; IGc1; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 10354 MW; 2F485A66B6532A61 CRC64;

Query Match 31.8%; Score 87; DB 7; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.9e-83;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 PPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGTQK 243
DB 1 PPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGTQK 60

QY 244 WAAVVPVSGEEQRYTCHVQHEGLPQPL 270
DB 61 WAAVVPVSGEEQRYTCHVQHEGLPQPL 87

RESULT 11
Q29958 PRELIMINARY; PRT; 316 AA.
ID Q29958
AC Q29958;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HLA-C protein (Fragment).
GN HLA-C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89122144; PubMed=2914713;
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RA Cianetti L., Testa U., Scotto L., La Valle R., Simeone A., Boccoli G.,
RA Giannella G., Peschle C., Borcinelli E.,
RT "Three new class I HLA alleles: structure of mRNAs and alternative
RT mechanisms of processing."
RL Immunogenetics 29:80-91(1989).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; M24096; AAA59654.1; -.
DR P.R; C37028; C37028.
DR HSP; P30685; 1A9B.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 316 AA; 35380 MW; C03B1EC87F75C9BA CRC64;
Query Match 26.6%; Score 73; DB 7; Length 316;
Best Local Similarity 100.0%; Pred. No. 6.5e-68;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 SDEATLRCWALGFYPAEITLTWQDGEQDTQDTLVELTRPAGDGTQKWAAVVPSGEE 254
DB 169 SDEATLRCWALGFYPAEITLTWQDGEQDTQDTLVELTRPAGDGTQKWAAVVPSGEE 228
QY 255 QRYTCHVQHEGLP 267
DB 229 QRYTCHVQHEGLP 241
RESULT 12
Q860F6 PRELIMINARY; PRT; 314 AA.
AC Q860F6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN MANE-A.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Lafont B.A.P.; Buckler-White A., Plishka R., Buckler C., Martin M.A.;
RT "The classical and non-classical MHC class I genes of pig-tailed
RT macaques (Macaca nemestrina)."
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY204730; AAC84319.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
QY 195 SDEATLRCWALGFYPAEITLTWQDGEQDTQDTLVELTRPAGDGTQKWAAVVPSGEE 254
DB 169 SDEATLRCWALGFYPAEITLTWQDGEQDTQDTLVELTRPAGDGTQKWAAVVPSGEE 228
QY 255 QRYTCHVQHEGLP 267
DB 229 QRYTCHVQHEGLP 241

DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 314 314
SQ SEQUENCE 314 AA; 35463 MW; C585496BA90BDC85 CRC64;
Query Match 22.6%; Score 62; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 191 HHPISDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVELTRPAGDGTQKWAAVVPSGEE 250
DB 183 HHPISDHEATLRCWALGFYPAEITLTWQDGEQDTQDTLVELTRPAGDGTQKWAAVVPSGEE 242
QY 251 SG 252
DB 243 SG 244
RESULT 13
Q9MXS7 PRELIMINARY; PRT; 353 AA.
AC Q9MXS7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MHC class I heavy chain antigen (Fragment).
GN MANU-A.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20260989; PubMed=10803844;
RA Urvater J.A.; McAdam S.N.; Loehrke J.H.; Allen T.M.; Moran J.L.;
RA Rowell T.J.; Rojo S.; Lopez de Castro J.A.; Taurag J.D.; Watkins D.I.;
RT "A high incidence of Shigella-induced arthritis in a primate species:
RT major histocompatibility complex class I molecules associated with
RT resistance and susceptibility, and their relationship to HLA-B*27.";
RL Immunogenetics 51:314-325(2000).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; AF157399; AAF71168.1; -.
DR HSP; P30685; 1A9B.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 353 AA; 39448 MW; EC1A0A7DB085F5B7 CRC64;
Query Match 22.3%; Score 61; DB 7; Length 353;
Best Local Similarity 100.0%; Pred. No. 3e-55;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 SDEATLRCWALGFYPAEITLTWQDGEQDTQDTLVELTRPAGDGTQKWAAVVPSGEE 254
DB 207 SDEATLRCWALGFYPAEITLTWQDGEQDTQDTLVELTRPAGDGTQKWAAVVPSGEE 266

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QY 255 Q 255
DB 267 Q 267

RESULT 14
Q9MXS6
ID Q9MXS6 PRELIMINARY; PRT; 353 AA.
AC Q9MXS6
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MHC class I heavy chain antigen (fragment).
GN MAMU-A.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20260989; PubMed=10803844;
RA Urvater J.A., McAdam S.N., Loehrke J.H., Allen T.M., Moran J.L.,
RA Rowell T.J., Rojo S., Lopez de Castro J.A., Taurag J.D., Watkins D.I.;
RT "A high incidence of Shigella-induced arthritis in a primate species:
RT major histocompatibility complex class I molecules associated with
RT resistance and susceptibility, and their relationship to HLA-B27."
RL Immunogenetics 51:314-325(2000).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AF157400; AAF71169.1; -.
DR HSSP; P30685; IA9E.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR GlycoProtein; Transmembrane.
KW NON_TER
SQ SEQUENCE 353 AA; 39387 MW; 4F1A6D397P71FEA3 CRC64;

Query Match 22.3%; Score 61; DB 7; Length 353;
Best Local Similarity 100.0%; Pred. No. 3e-55;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 SDHEATLRGKALGFYPAEITLTWQDGEQDTDELVETRPAGDGTQKAAVVPVSGEE 254
DB 207 SDHEATLRGKALGFYPAEITLTWQDGEQDTDELVETRPAGDGTQKAAVVPVSGEE 266

QY 255 Q 255
DB 267 Q 267

RESULT 15
Q9MXS5
ID Q9MXS5 PRELIMINARY; PRT; 365 AA.
AC Q9MXS5
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MHC class I heavy chain antigen.
GN MAMU-A.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20260989; PubMed=10803844;
RA Urvater J.A., McAdam S.N., Loehrke J.H., Allen T.M., Moran J.L.,
RA Rowell T.J., Rojo S., Lopez de Castro J.A., Taurag J.D., Watkins D.I.;
RT "A high incidence of Shigella-induced arthritis in a primate species:
RT major histocompatibility complex class I molecules associated with
RT resistance and susceptibility, and their relationship to HLA-B27."
RL Immunogenetics 51:314-325(2000).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AF157400; AAF71169.1; -.
DR HSSP; P30685; IA9E.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR GlycoProtein; Transmembrane.
KW NON_TER
SQ SEQUENCE 365 AA; 40772 MW; 5B7D7D45B8BC284C CRC64;

Query Match 22.3%; Score 61; DB 7; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.1e-55;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 SDHEATLRGKALGFYPAEITLTWQDGEQDTDELVETRPAGDGTQKAAVVPVSGEE 254
DB 219 SDHEATLRGKALGFYPAEITLTWQDGEQDTDELVETRPAGDGTQKAAVVPVSGEE 278

QY 255 Q 255
DB 279 Q 279

Search completed: June 18, 2004, 19:31:21
Job time : 46 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:26:37 ; Search time 17 seconds
(without alignments)

839.248 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRYSTAVSRPGRGP.....QRYTCHVQHEGLPOLILRW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 segs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	362	1	HLAF_HUMAN
2	136	46.0	346	1	LC28_PANTR
3	59	21.5	348	1	HLAF_MACMU
4	44	16.1	362	1	HLAF_HUMAN
5	44	16.1	365	1	LA01_HUMAN
6	44	16.1	365	1	LA01_PANTR
7	44	16.1	365	1	LA03_HUMAN
8	44	16.1	365	1	LA03_PANTR
9	44	16.1	365	1	LA04_PANTR
10	44	16.1	365	1	LA11_HUMAN
11	44	16.1	365	1	LA23_HUMAN
12	44	16.1	365	1	LA24_HUMAN
13	44	16.1	365	1	LA30_HUMAN
14	44	16.1	365	1	LA36_HUMAN
15	44	16.1	366	1	LC02_HUMAN
16	44	16.1	366	1	LC03_HUMAN
17	44	16.1	366	1	LC04_HUMAN
18	44	16.1	366	1	LC05_HUMAN
19	44	16.1	366	1	LC06_HUMAN
20	44	16.1	366	1	LC08_HUMAN
21	44	16.1	366	1	LC12_HUMAN
22	44	16.1	366	1	LC14_HUMAN
23	44	16.1	366	1	LC15_HUMAN
24	44	16.1	366	1	LC16_HUMAN
25	44	16.1	366	1	LC18_HUMAN
26	43	15.7	358	1	HLAE_PONPY
27	40	14.6	359	1	HLAE_PONPY
28	39	14.2	338	1	HLAF_HUMAN
29	37	13.5	365	1	LC01_GORGO
30	32	11.7	359	1	LB01_PANTR
31	32	11.7	362	1	LA02_PANTR
32	32	11.7	362	1	LB01_GORGO
33	32	11.7	362	1	LB02_GORGO

ALIGNMENTS

RESULT 1

ID	HLAF_HUMAN	STANDARD;	PRT;	362 AA.
AC	P30511;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (leukocyte antigen F) (CDA12).			
GN	HLA-F OR HLAF OR HLA-S.4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90111605; PubMed=1688605;			
RA	Geraghty D.E., Wei X., Orr H.T., Koller B.H.;			
RT	"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive element."			
RT	J. Exp. Med. 171:1-18(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91197889; PubMed=1707659;			
RA	Lury D., Epstein H., Holmes N.;			
RT	"The human class I MHC gene HLA-F is expressed in lymphocytes."			
RL	Int. Immunol. 2:531-537(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Shiina S., Tamiya G., Oka A., Inoko H.;			
RT	"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.			
CC	-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; X17093; CAA34947.1; -.			
DR	EMBL; AP000521; BAB63337.1; -.			
DR	PIR; A60384; A60384.			
DR	HSSP; Q30201; IAE2.			
DR	Gene; HGNC:4963; HLA-F.			
DR	MIM; 143110; -.			
DR	GO; GO:0030106; F:MHC class I receptor activity; TAS.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG_MHC.			

P13751 pan troglod
P30381 gorilla gor
P01899 homo sapien
P30460 homo sapien
P30461 homo sapien
P30462 homo sapien
P30464 homo sapien
P30466 homo sapien
P30989 homo sapien
P18463 homo sapien
Q95365 homo sapien
P30475 homo sapien

34 32 11.7 362 1 LB02_PANTR
35 32 11.7 362 1 LB03_GORGO
36 32 11.7 362 1 LB07_HUMAN
37 32 11.7 362 1 LB08_HUMAN
38 32 11.7 362 1 LB13_HUMAN
39 32 11.7 362 1 LB14_HUMAN
40 32 11.7 362 1 LB15_HUMAN
41 32 11.7 362 1 LB18_HUMAN
42 32 11.7 362 1 LB27_HUMAN
43 32 11.7 362 1 LB37_HUMAN
44 32 11.7 362 1 LB38_HUMAN
45 32 11.7 362 1 LB39_HUMAN


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DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR SMART; SM00407; IG; 1.
DR PRODOM; PD000050; MHC_I; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 362
FT
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN F.
FT DOMAIN 22 111
FT DOMAIN 112 203
FT DOMAIN 204 295
FT DOMAIN 296 305
FT DOMAIN 306 329
FT TRANSMEM 330 362
FT DOMAIN 330 362
FT DISULFID 122 185
FT DISULFID 224 280
FT CARBOHYD 107 107
SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Query Match 100.0%; Score 274; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.8e-279; Indels 0; Gaps 0;
Matches 274; Conservative 0; Mismatches 0;

Qy 1 GSHSLRYFSTAVSRPGEGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWQEGPQYW 60
Db 22 GSHSLRYFSTAVSRPGEGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWQEGPQYW 81

Qy 61 EWTGYAKANAQTDRLVALNLLRRYNSQSGSHTLQNGCGDMPDGLRLRGYHQHAYDG 120
Db 82 EWTGYAKANAQTDRLVALNLLRRYNSQSGSHTLQNGCGDMPDGLRLRGYHQHAYDG 141

Qy 121 KDYISLNEDLSRWTAAADTVQAQITQRFYEAEBEYAEFFTYLEGECELELLRRYLENGKETLQ 180
Db 142 KDYISLNEDLSRWTAAADTVQAQITQRFYEAEBEYAEFFTYLEGECELELLRRYLENGKETLQ 201

Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEPRPADGDT 240
Db 202 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEPRPADGDT 261

Qy 241 FOKAAVVPVSGERQRYTCHVQHEGLPQLRLRW 274
Db 262 FOKAAVVPVSGERQRYTCHVQHEGLPQLRLRW 295

RESULT 2
1C28 PANTR
ID 1C28 PANTR STANDARD; PRT; 346 AA.
AC P16215;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CHLA class I histocompatibility antigen, CH28 alpha chain precursor.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90201944; PubMed=1690682;
RA Lawlor D.A., Warren E., Ward F.E., Parham P.;
RT "Comparison of class I MHC alleles in humans and apes.";
RL Immunol. Rev. 113:147-185(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88319000; PubMed=3412487;
RA Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.;
RT "HLA-A and B polymorphisms predate the divergence of humans and
RT chimpanzees.";
RL Nature 335:268-271(1988).

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CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC HESBL; M30685; AA87973.1; -
CC HESBL; Q30201; 1A6Z.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003597; IG_c1.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; IG; 1.
CC Pfam; PF00129; MHC_I; 1.
CC PRINTS; PR01638; MHCCLASSI.
CC PRODOM; PD000050; MHC_I; 1.
CC SMART; SM00407; IG; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 346
FT
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT CH28 ALPHA CHAIN.
FT DOMAIN 22 111
FT DOMAIN 112 203
FT DOMAIN 204 295
FT DOMAIN 296 305
FT TRANSMEM 306 329
FT DOMAIN 330 346
FT DISULFID 122 185
FT DISULFID 224 280
FT CARBOHYD 107 107
SQ SEQUENCE 346 AA; 39084 MW; F83E882D5C2E0971 CRC64;

Query Match 46.0%; Score 126; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.4e-124;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 TTGYAKANAQTDRLVALNLLRRYNSQSGSHTLQNGCGDMPDGLRLRGYHQHAYDGKD 122
Db 84 TTGYAKANAQTDRLVALNLLRRYNSQSGSHTLQNGCGDMPDGLRLRGYHQHAYDGKD 143

Qy 123 YISLNEDLSRWTAAADTVQAQITQRFYEAEBEYAEFFTYLEGECELELLRRYLENGKETLQRA 182
Db 144 YISLNEDLSRWTAAADTVQAQITQRFYEAEBEYAEFFTYLEGECELELLRRYLENGKETLQRA 203

Qy 183 DPPKAH 188
Db 204 DPPKAH 209

RESULT 3
HLAF_MACMU
ID HLAF_MACMU STANDARD; PRT; 348 AA.
AC P33617;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F
DE antigen) (leukocyte antigen F).
GN HLA-F OR HLAF.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;

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RN SEQUENCE FROM N.A.
RX MEDLINE=93246295; PubMed=8482576;
RA Otting N., Bontrop R.E.;
RT "Characterization of the rhesus macaque (Macaca mulatta) equivalent
of HLA-F.";
RL Immunogenetics 38:141-145(1993).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z21819; CAA79885.1; -
DR PIR; S29990; S29990.
DR HSSP; Q30201; IA6Z.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_I.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS08335; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 348
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN F.
FT DOMAIN 22 113
FT DOMAIN 114 205
FT DOMAIN 206 297
FT DOMAIN 298 307
FT DOMAIN 308 331
FT TRANSMEM 332 348
FT DISULFID 124 187
FT DISULFID 226 282
FT CARBOHYD 109 109
FT SEQUENCE 348 AA; 39300 MW; 77BD7E3B9B11E0F7 CRC64;
Query Match 21.5%; Score 59; DB 1; Length 348;
Best Local Similarity 100.0%; Pred. No. 6.8e-54;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 212 EITLTWRDGEETQDTVELVETPAGDGTGFKWAAVVPVSGEQRVYTCVHQEGLPQL 270
DB 235 EITLTWRDGEETQDTVELVETPAGDGTGFKWAAVVPVSGEQRVYTCVHQEGLPQL 293
RESULT 4
HLAH HUMAN STANDARD; PRT; 362 AA.
AC P01893;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, alpha chain H precursor
DE (HLA-AR) (HLA-12.4).
GN HLA-H OR HLAH
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=92151002; PubMed=6461010;
RA Malissen M., Malissen B., Jordan B.R.;
RT "Exon/intron organization and complete nucleotide sequence of an HLA
gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00191; AAA36218.1; ALT_INIT.
DR HSSP; P03989; IHSA.
DR Genew; HGNC:4965; HLA-H.
DR XIM; 142800; -
DR GO; GO:0005887; C: integral to plasma membrane; NAS.
DR GO; GO:0030106; F: MHC class I receptor activity; NAS.
DR GO; GO:0006955; P: immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS08335; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN H.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40850 MW; 0BCDAE8D61A81B86 CRC64;
Query Match 16.1%; Score 44; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 QTQDTVELVETPAGDGTGFKWAAVVPVSGEQRVYTCVHQEGLP 267
DB 248 QTQDTVELVETPAGDGTGFKWAAVVPVSGEQRVYTCVHQEGLP 291
RESULT 5
LA01 HUMAN STANDARD; PRT; 365 AA.
ID LA01 HUMAN
AC P30433; O77964; O78171; Q9MYA3; Q9TP25; Q9TP5;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, A-1 alpha chain precursor
DE (MHC class I antigen A*1).
GN HLA-A OR HLAH
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
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NCBI_TaxID=9606;
RA [1] SEQUENCE FROM N.A. (A*0101).
RP MEDLINE=88234547; PubMed=3375250;
RX Parham P., Lomen C.E., Lawlor D.A., Ways J.P., Holmes N., Coppin H.L.,
RA Salter R.D., Wan A.M., Ennis P.D.;
RT "Nature of polymorphism in HLA-A, -B, and -C molecules.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:4005-4009(1988).
RN [2]
RP SEQUENCE FROM N.A. (A*0101).
RX MEDLINE=89235215; PubMed=2715640;
RA Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
RT "Diversity and diversification of HLA-A,B,C alleles.";
RL J. Immunol. 142:3937-3950(1989).
RN [3]
RP SEQUENCE FROM N.A. (A*0101).
RA Warren E.;
RL Submitted (APR-1989) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (A*0101).
RX MEDLINE=91067475; PubMed=2251137;
RA Girdlestone J.;
RT "Nucleotide sequence of an HLA-A1 gene.";
RL Nucleic Acids Res. 18:6701-6701(1990).
RN [5]
RP SEQUENCE FROM N.A. (A*0101).
RX MEDLINE=98007773; PubMed=9349617;
RA Laforet M., Froelich N., Parisiadis A., Pfeiffer B., Schell A.,
RA Falier B., Woehl-Jaegle M.L., Cazenave J.P., Tongio M.M.;
RT "A nucleotide insertion in exon 4 is responsible for the absence of
expression of an HLA-A*01 allele.";
RL Tissue Antigens 50:347-350(1997).
RN [6]
RP SEQUENCE FROM N.A. (A*0101).
RA Waller M.J., Robinson J., Marsh S.G.E.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (A*0101).
RC TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan T.B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE FROM N.A. (A*0102).
RX MEDLINE=95282145; PubMed=7761977;
RA Browning M.J., Madrigal J.A., Krausa P., Kowalski H.,
RA Allsopp C.E., Little A.-M., Turner S., Adams E.J., Arnett K.L.,
RA Bodmer W.F., Parham P.;
RT "The HLA-A,B,C genotype of the class I negative cell line Daudi
reveals novel HLA-A and -B alleles.";
RL Tissue Antigens 45:177-187(1995).
RN [9]
RP SEQUENCE OF 26-206 FROM N.A. (A*0103).
RX MEDLINE=98101100; PubMed=9438203;
RA Sitha S., Scheltinga S.A., Johnston-Dow L.A., White C.B.,
der van Zwan A.W., Bakema J.E., Rozemuller E.H., van der Tweel J.G.,
RA Kronink M.N., Tilanus M.G.J.;
RT "A generic sequencing based typing approach for the identification of
HLA-A diversity.";
RL Hum. Immunol. 57:120-128(1997).
RN [10]
RP SEQUENCE OF 26-206 FROM N.A. (A*0103).
RC TISSUE=Blood;
RX MEDLINE=21100775; PubMed=11182232;
RA Poland G.A., Sohni Y., Domanic M., Kroning C.M., DeGoey S.R.,
RA Jimale M., Jacobson R.M., Moore S.B.;
RT "High frequency of HLA-A*0103 allele in a Somali population.";
RL Hum. Immunol. 62:197-200(2001).
RN [11]
RP SEQUENCE OF 26-206 FROM N.A. (A*0106).
RX MEDLINE=20309230; PubMed=10852390;
RA Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester R.,
RA NG J., Hartzman R.J., Hurley C.K.;
RT "Seventeen more novel HLA-A locus alleles.";
RL Tissue Antigens 55:369-373(2000).
RN [12]
RP SEQUENCE OF 26-206 FROM N.A. (A*0107).
RX Tamouza R., Fortier C., Mahfoudh N., Schaeffer V., Poirier J.C.,
RA Marzais F., Gautreau C., Charron D.;
RT "A new HLA-A*01 allele.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SULFATION.
RX MEDLINE=88088800; PubMed=3121736;
RA Sant A.J., Zacheis M., Rumbarger T., Giacoletto K.S., Schwartz B.D.;
RT "Human Ia alpha- and beta-chains are sulfated.";
RL J. Immunol. 140:155-160(1988).
CC -1- FUNCTION: Involved in the presentation of foreign antigens to
the immune system.
CC -1- SUBUNIT: Dimer of alpha chain and a beta chain (beta-2-
microglobulin).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: Sulfated.
CC -1- POLYMORPHISM: The following alleles of A-1 are known: A*0101,
A*0102, A*0103, A*0106 and A*0107. The sequence shown is that of
A*0101.

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EMBL; M24043; AAA59652.1; -
EMBL; X55710; CAA39243.1; -
EMBL; Z93949; CAB07989.1; -
EMBL; AJ278305; CAB93537.1; -
EMBL; BC003069; AAH03069.1; -
EMBL; U07161; AAA80569.1; -
EMBL; Y12469; CAA73072.1; -
EMBL; Y12470; CAA73073.1; -
EMBL; AF214112; AAF19525.1; -
EMBL; AF214111; AAF19525.1; JOINED.
EMBL; AF143322; AAD33894.1; -
EMBL; AF143323; AAD33894.1; JOINED.
EMBL; AF219633; AAF73862.1; -
EMBL; AF219632; AAF73862.1; JOINED.
PIR; I38518; I38518.
PIR; I61856; I61856.
HSP; O19673; IHSB.
Genew; HGNC:4931; HLA-A.
MIN; 142800; -
GO; GO:0005887; C: integral to plasma membrane; NAS.
GO; GO:0030106; F: MHC class I receptor activity; NAS.
GO; GO:0006955; P: immune response; NAS.
InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR001039; MHC I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGI1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-1 ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CYTOPLASMIC TAIL.
FT MOD RES 83 83
FT CARBOHYD 110 110
FT DISULFID 125 188
FT VARIANT 227 283
FT VARIANT 33 33
FT FTTid=VAR_004332. A*0102).
FT R -> S (in allele A*0102).
FT /FTid=VAR_004333.
FT G -> R (in allele A*0107).
FT /FTid=VAR_016719.
FT M -> V (in allele A*0107).
FT /FTid=VAR_016720.
FT A -> E (in allele A*0107).
FT /FTid=VAR_016721.
FT D -> A (in allele A*0107).
FT /FTid=VAR_016722.
FT I -> M (in allele A*0103).
FT /FTid=VAR_016723.
FT R -> L (in allele A*0106).
FT /FTid=VAR_016724.
FT V -> A (in allele A*0106).
FT /FTid=VAR_016725.
FT SEQUENCE 365 AA; 40846 MW; 8667AFF3F06C4932 CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 QTQDTLVELTRPAGDGTQKWAADVVPVSGEQRVYCHVQHEGLP 267
DB 248 QTQDTLVELTRPAGDGTQKWAADVVPVSGEQRVYCHVQHEGLP 291

RESULT 6
ID 1A01 PANTR STANDARD; PRT; 365 AA.
AC P16209;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE "HLA class I histocompatibility antigen, A-2 alpha chain precursor.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90201944; PubMed=1690682;
RA Lawlor D.A., Warren E., Ward F.E., Parham P.;
RT "Comparison of class I MHC alleles in humans and apes.";
RL Immunol. Rev. 113:147-185(1990).
RL FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.

-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
-----
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-----
EMBL; M30678; AAA87970.1; --
DR PIR; I36961; I36961.
DR HSP; Q95352; IHHK.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR001039; MHC I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGI1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 365
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-2 ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CYTOPLASMIC TAIL.
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT SEQUENCE 365 AA; 40848 MW; FC452786BD038D3E CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 QTQDTLVELTRPAGDGTQKWAADVVPVSGEQRVYCHVQHEGLP 267
DB 248 QTQDTLVELTRPAGDGTQKWAADVVPVSGEQRVYCHVQHEGLP 291

RESULT 7
ID 1A03 HUMAN STANDARD; PRT; 365 AA.
AC P04439; O19546; O9GJ66; Q9GJ67; Q9GJ68; Q9MYG4; Q9TPR8;
DT 13-AUG-1987 (Rel. 05, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE "HLA class I histocompatibility antigen, A-3 alpha chain precursor
(MHC class I antigen A*3).
GN HLA-A OR HLA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*0301).
RX MEDLINE=84207948; PubMed=6609814;
RA Strachan T., Sodoyer R., Damotte M., Jordan B.R.;
RT "Complete nucleotide sequence of a functional class I HLA gene,
HLA-A*3; implications for the evolution of HLA genes.";
RL EMBO J. 3:887-894(1984).
RN [2]
RP SEQUENCE FROM N.A. (A*0301).
RA Ellsexon M.E., Hildebrand W.H.;
```

Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A. (A*0301).
RA Shima S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A. (A*0302).
RP MEDLINE=85290871; PubMed=2993417;
RX Cowan E.P., Jordan B.E., Colligan J.E.;
RA "Molecular cloning and DNA sequence analysis of genes encoding
RT cytotoxic T lymphocyte-defined HLA-A3 subtypes: the E1 subtype."
RL J. Immunol. 135:2835-2841(1985).
[5]
SEQUENCE FROM N.A. (A*0302).
RP Bettinotti M.P., Hadzikadic L., Adams S., Marincola F.M.;
RA "Complete coding sequence of HLA-A*0302."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE OF 1-341 FROM N.A. (A*0304).
RP MEDLINE=99180630; PubMed=10079303;
RX Santos S., Balas A., Garcia-Sanchez F., Lillo R., Merino J.L.,
RA Vicario J.L.;
RT "Complete cDNA coding sequence of a new HLA-A3 subtype (A*0304) with a
RL new HLA polymorphism at exon 3."
RL Immunogenetics 49:360-361(1999).
[7]
SEQUENCE OF 26-206 FROM N.A. (A*0305).
RP Becher M.P., Wu J., Williams T.;
RA "Novel human HLA-A alleles identified in potential bone marrow
RT donors."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[8]
SEQUENCE OF 26-298 FROM N.A. (A*0305).
RP TISSUE=Blood;
RA Poli F., Frison S., Crespiatico L., Longhi E.;
RT "Identification of a HLA-A*03 new variant."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the presentation of foreign antigens to
CC the immune system.
CC -!- SUBUNIT: Dimer of alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- POLYMORPHISM: The following alleles of A-3 are known: A*0301
CC (A-3.1), A*0302, A*0304 and A*0305. The sequence shown is that of
CC A*0301.
CC
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CC
CC EMBL; X00492; CAA25162.1; ALT SEQ.
CC EMBL; U32184; AAB63980.1; -.
CC EMBL; AP000520; BAB63400.1; -.
CC EMBL; AP000519; BAB63400.1; JOINED.
CC EMBL; AF217561; AAF28734.1; -.
CC EMBL; AF015330; AAB66582.1; -.
CC EMBL; AF190719; AAF03243.1; -.
CC EMBL; AF190718; AAF03243.1; JOINED.
CC EMBL; AF401085; CAC06086.1; -.
CC EMBL; AJ401086; CAC06087.1; -.
CC EMBL; AJ401087; CAC06088.1; -.
CC F01; A02192; HLHUA3.
CC HSSP; C19673; IHSB.
CC Genew; HGNC:4931; HLA-A.
CC MIM; 142800; -.
CC GO; GO:0005887; C:integral to plasma membrane; NAS.
CC GO; GO:0030106; F:MHC class I receptor activity; NAS.
CC GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_1; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 A-3 ALPHA CHAIN.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 365 CYTOPLASMIC TAIL.
FT DISULFID 120 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT DISULFID 227 283 BY SIMILARITY.
FT VARIANT 176 176 E -> V (in allele A*0302).
FT VARIANT 180 180 L -> Q (in allele A*0302).
FT VARIANT 185 185 D -> E (in allele A*0305).
FT VARIANT 199 199 /FTID=VAR_016604.
FT VARIANT 319 319 G -> R (in allele A*0304).
FT CONFLICT 319 319 /FTID=VAR_016605.
FT SEQUENCE 365 AA; 40840 MW; DEDFCBC4450B0580 CRC64;
Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-39;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 QTQDTLVETRPAGDGTQKNAVVVPSGEQRVTCHVQHEGLP 267
DB 248 QTQDTLVETRPAGDGTQKNAVVVPSGEQRVTCHVQHEGLP 291
RESULT 8
1A03 PANTR STANDARD; PRT; 365 AA.
ID 1A03 PANTR STANDARD; PRT; 365 AA.
AC P13748.
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CHLA class I histocompatibility antigen, A-108 alpha chain precursor.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OC NCBI_Taxid=9596;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89030641; PubMed=2460344;
RA Mayer W.E., Jonker M., Klein D., Ivanyi P., van Seventer G.,
RA Klein J.;
RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
RT trans-species mode of evolution."
RL EMBO J. 7:2765-2774(1988).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC
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CC or send an email to license@isb-sib.ch).
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DR EMBL; X13113; CAA31505.1; ALT_INIT.
DR PIR; S019673; IHSB.
DR HSSP; O19673; IHSB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 365
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-108 ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CYTOPLASMIC TAIL.
FT DISULFID 125 188
FT BY SIMILARITY.
FT DISULFID 227 283
FT N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT CARBOHYD 110 110
SQ SEQUENCE 365 AA; 40822 MW; 48CC75055221FC3 CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVEVTRPAGDGTGFKAAVAVVPSGEEQRYTCHVQHEGLP 267
DB 248 QTQDTLVEVTRPAGDGTGFKAAVAVVPSGEEQRYTCHVQHEGLP 291

RESULT 9
1A04 PANTR STANDARD; PRT; 365 AA.
AC P13749;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CHLA class I histocompatibility antigen, A-126 alpha chain precursor.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
[1]_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89030641; PubMed=2460344;
RA Mayer W.E., Jonker M., Klein D., Ivanyi P., van Seventer G.,
RA Klein J.;
RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
trans-species mode of evolution.";
RL EMBL J. 7:2765-2774(1988).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC use by non-profit institutions as long as its content is in no way
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DR EMBL; X13114; CAA31506.1; -.
DR PIR; S01171; S01171.
DR HSSP; O19673; IHSB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 365
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-126 ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CYTOPLASMIC TAIL.
FT DISULFID 125 188
FT BY SIMILARITY.
FT DISULFID 227 283
FT N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT CARBOHYD 110 110
SQ SEQUENCE 365 AA; 40656 MW; D3C9A810B22A768F CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVEVTRPAGDGTGFKAAVAVVPSGEEQRYTCHVQHEGLP 267
DB 248 QTQDTLVEVTRPAGDGTGFKAAVAVVPSGEEQRYTCHVQHEGLP 291

RESULT 10
1A11 HUMAN STANDARD; PRT; 365 AA.
AC P13746; O19605; Q29747; Q29835; Q9ECN0; Q9MYI5; Q9TQE9;
AC Q9TQP6; Q9TQP7;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, A-11 alpha chain precursor
DE (MHC class I antigen A*11).
GN HLA-A OR HLA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*1101 AND A*1102).
RX MEDLINE=89030641; PubMed=2460344;
RA Mayer W.E., Jonker M., Klein D., Ivanyi P., van Seventer G.,
RA Klein J.;
RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
trans-species mode of evolution.";
RL EMBL J. 7:2765-2774(1988).
CC [2]
RP SEQUENCE FROM N.A. (A*1101 AND A*1102).
RX MEDLINE=94287401; PubMed=8016845;
RA Lin L., Tokunaga K., Ishikawa Y., Bannai M., Kashiwase K.,
RA Kuwata S., Akaza T., Tadokoro K., Shibata Y., Juji T.;
RT "Sequence analysis of serological HLA-A11 split antigens, All.1 and
All.2.";
RL Tissue Antigens 43:78-82(1994).
CC [3]
RP SEQUENCE OF 26-365 FROM N.A. (A*1101).
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FT VARIANT 345 345 T -> S (in allele A*1105).
FT /FTID=VAR_016736.
SQ SEQUENCE 365 AA; 40937 MW; FE449CE2D4B6FC5 CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTGFKWAAVVPVSGEQRVTCHVOHEGLP 267
DB 248 QTQDTLTVETRPAGDGTGFKWAAVVPVSGEQRVTCHVOHEGLP 291

RESULT 11
1A23_HUMAN STANDARD; PRT; 365 AA.
AC P30447; Q9QF1; Q9TQF8; Q9TQF5; Q9TQF6;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, A-23 alpha chain precursor
DE (MHC class I antigen A*23) (A-9).
GN HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A. (A*2301).
RA Little A.-M., Madrigal J.A., Parham P.;
RT "Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
RL Immunogenetics 35:41-45(1992).
RN [2]
RS SEQUENCE OF 26-206 FROM N.A. (A*2302 AND A*2303).
RA Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester R.,
RA Ng J., Hartzman R.J., Hurley C.K.;
RT "Seventeen more novel HLA-A locus alleles.";
RL Tissue Antigens 55:369-373(2000).
RN [3]
RS SEQUENCE OF 26-206 FROM N.A. (A*2304 AND A*2305).
RA Steiner N.K., Edson S.M., Mitton W., Ng J., Hartzman R.J.,
RA Hurley C.K.;
RT "Seven novel HLA-A alleles carry previously observed polymorphisms.";
RL Tissue Antigens 56:1551-552(2000).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to
CC the immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- POLYMORPHISM: The following alleles of A-23 are known: A*2301, of
CC A*2302, A*2303, A*2304 and A*2305. The sequence shown is that of
CC A*2301.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M64742; AAA03662.1; -
CC EMBL; AF137080; AAD33736.1; -
CC EMBL; AF137079; AAD33736.1; JOINED.
CC EMBL; AF102572; AAD28171.1; -
CC EMBL; AF102571; AAD28171.1; JOINED.
CC EMBL; AF135548; AAD22272.1; -
CC EMBL; AF135549; AAD22272.1; JOINED.
CC EMBL; AF140860; AAD31878.1; -
CC EMBL; AF140859; AAD31878.1; JOINED.
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DR HSPSP; Q95352; IHHK.
DR Genew; HGNC:4931; HLA-A.
DR MIM; 142800; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGG1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 A-23 ALPHA CHAIN.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 365 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 Y -> C (in allele A*2305).
FT VARIANT 31 31 /FTID=VAR_016606.
FT VARIANT 151 151 K -> N (in allele A*2303).
FT VARIANT 180 180 /FTID=VAR_016607.
FT VARIANT 180 180 L -> W (in allele A*2302).
FT VARIANT 190 191 /FTID=VAR_016608.
FT VARIANT 190 191 DG -> EW (in allele A*2304).
FT /FTID=VAR_016609.
SQ SEQUENCE 365 AA; 40732 MW; C372DE503BF393D0 CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTGFKWAAVVPVSGEQRVTCHVOHEGLP 267
DB 248 QTQDTLTVETRPAGDGTGFKWAAVVPVSGEQRVTCHVOHEGLP 291

RESULT 12
1A24_HUMAN STANDARD; PRT; 365 AA.
AC P05534; P30448; P30449; Q29908; Q29909; Q29910; Q95355;
DT 01-NOV-1988 (Rel. 09, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE HLA class I histocompatibility antigen, A-24 alpha chain precursor
DE (MHC class I antigen A*24) (A-9).
GN HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A. (A*2401).
RX MEDLINE=85206128; PubMed=2387115;
RA N'Guyen C., Sodoyer R., Trucy J., Strachan T., Jordan B.R.;
RT "The HLA-AW24 gene: sequence, surroundings and comparison with the
RT HLA-A2 and HLA-A3 genes.";
RL Immunogenetics 21:479-489(1985).
RN [2]
RS REVISIONS.
RA Jordan B.R.;
RL Submitted (XXX-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RS SEQUENCE FROM N.A. (A*2402 AND A*2403).
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RX MEDLINE=92104637; PubMed=1729171;
RA Little A.-M., Madrigal J.A., Parham P.;
RT Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3." ;
RL Immunogenetics 35:41-45(1992).
RN [4]
RP SEQUENCE FROM N.A. (A*2402).
RX MEDLINE=92269955; PubMed=1317015;
RA Belich M.P., Madrigal J.A., Hilgeland W.H., Zemmour J.,
RT Williams R.C., Luz R., Petzl-Erler M.L., Parham P.;
RL "Unusual HLA-B alleles in two tribes of Brazilian Indians." ;
RN Nature 357:326-329(1992).
RX [5]
RP SEQUENCE FROM N.A. (A*2402).
RX MEDLINE=98007772; PubMed=9349616;
RA Laforet M., Froelich N., Parissiadis A., Bausinger H., Pfeiffer B.,
RT Tongio M.M.;
RL "An intronic mutation responsible for a low level of expression of an
RT HLA-A*24 allele." ;
RL Tissue Antigens 50:340-346(1997).
RN [6]
RP SEQUENCE FROM N.A. (A*2408).
RX TISSUE=Blood;
RA Kashiwase K., Tokunaga K., Ishikawa Y., Qiu L., Furuya M.,
RT Sawanaka K., Akaza T., Tadokoro K., Juji T.;
RL "A new A9 sequence HLA-A9RH from Japanese." ;
RL MHC 3:9-14(1996).
RX [7]
RP SEQUENCE OF 26-206 FROM N.A. (A*2410).
RX TISSUE=Blood;
RA Gao X., Matheson B.;
RL MEDLINE=97161044; PubMed=9008316;
RT "A novel HLA-A*24 (A*2410) identified in a Javanese population." ;
RL Tissue Antigens 48:711-713(1996).
RN [8]
RP SEQUENCE OF 26-206 FROM N.A. (A*2406; A*2413 AND A*2414).
RX TISSUE=Blood;
RA Gao X., Lester S., Matheson B., Boettcher B., McCluskey J.;
RT "Three newly identified A*24 alleles: A*2406, A*2413 and A*2414." ;
RL Tissue Antigens 50:192-196(1997).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to
CC the immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- POLYMORPHISM: The following alleles of A-24 are known: A*2401,
CC A*2402, A*2403, A*2406, A*2408 (A9RH), A*2410 (A*24UV), A*2413
CC (A*24YM) and A*2414 (A*24SA). Allele A*2402 is represented in all
CC major racial groups. Allele A*2406 and allele A*2413 are found in
CC the Australian Aboriginal population. Allele A*2414 is found in
CC individuals of South American descent. The sequence shown is that
CC of A*2402.
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CC -----
DR EMBL; M15497; AAA59611.1; -
DR EMBL; M64740; AAA59600.1; -
DR EMBL; M64741; AAA59601.1; -
DR EMBL; Z72422; CAA96532.1; -
DR EMBL; D83516; BAA11936.1; -
DR EMBL; U37111; AAA83264.1; -
DR EMBL; U37110; AAA83264.1; JOINED.
DR EMBL; U37113; AAA83265.1; -
DR EMBL; U37112; AAA83265.1; JOINED.
DR EMBL; U37115; ABA40048.1; -
DR EMBL; U37114; ABA40048.1; JOINED.
DR EMBL; U19733; AAB60651.1; -

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DR EMBL; U18987; AAB60651.1; JOINED.
DR PIR; I54416; I54416.
DR HSSP; Q95352; 1HHK.
DR Genew; HGNC:4931; HLA-A.
DR MIM; 142800; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; IG; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl_1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365
FT FT
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-24 ALPHA CHAIN.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT TRANSMEM 333 365
FT DOMAIN 110 110
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT VARIANT 5 5
FT VARIANT 27 27
FT VARIANT 86 86
FT VARIANT 89 89
FT VARIANT 119 119
FT VARIANT 121 121
FT VARIANT 123 123
FT VARIANT 131 131
FT VARIANT 180 180
FT VARIANT 180 180
FT VARIANT 187 187
FT VARIANT 190 191
FT FT
FT FTID=VAR_004359.
FT T -> A (in allele A*2401).
FT /FTID=VAR_004360
FT SEQUENCE 365 AA; 40688 MW; D33684DI28F9BEC3 CRC64;

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Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 224 QTQDTLTVTRPAGDGTFOKWAIVVPSGEORYTCHVQHEGLP 267
DB 248 QTQDTLTVTRPAGDGTFOKWAIVVPSGEORYTCHVQHEGLP 291

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RESULT 13

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1A30_HUMAN
ID 1A30_HUMAN STANDARD; PRT; 365 AA.
AC P16188; O19598; O62921; P30452; Q9UIP7;
DC 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

```

10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, A*30 alpha chain precursor
(MHC class I antigen A*30).
HLA-A OR HLA-A.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (A*3001).
MEDLINE=90038496; PubMed=2478623;
Kato K., Trapani J.A., Allopenna J., Dupont B., Yang S.Y.;
"Molecular analysis of the serologically defined HLA-Aw19 antigens. A
genetically distinct family of HLA-A antigens comprising A29, A31,
A32, and Aw33, but probably not A30.";
J. Immunol. 143:3371-3378(1989).
[2]
SEQUENCE FROM N.A. (A*3001).
MEDLINE=95176329; PubMed=7871528;
Olerup O., Daniels T.J., Baxter-Lowe L.;
"Correct sequence of the A*3001 allele obtained by PCR-SSP typing and
automated nucleotide sequencing.";
Tissue Antigens 44:265-267(1994).
[3]
SEQUENCE FROM N.A. (A*3002).
MEDLINE=93056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
"Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion.";
J. Immunol. 149:3411-3415(1992).
[4]
SEQUENCE OF 25-279 FROM N.A. (A*3003).
MEDLINE=93209813; PubMed=8458735;
Choo S.Y., Starling G.C., Anasetti C., Hansen J.A.;
"Selection of an unrelated donor for marrow transplantation
facilitated by the molecular characterization of a novel HLA-A
allele.";
Hum. Immunol. 36:20-26(1993).
[5]
SEQUENCE FROM N.A. (A*3004).
MEDLINE=96058597; PubMed=8522453;
Krausa P., Carcassi C., Orru S., Bodmer J.G., Browning M.J., Contu L.;
"Defining the allelic variants of HLA-A30 in the Sardinian population
using amplification refractory mutation system -- polymerase chain
reaction.";
Hum. Immunol. 44:35-42(1995).
[6]
SEQUENCE OF 26-206 FROM N.A. (A*3004).
MEDLINE=96435464; PubMed=8838350;
Lienert K., Russ G., Bennett G., Gao X., McCluskey J.;
"HLA-A*3004: a new A30 allele identified in an Australian Caucasian
population.";
Tissue Antigens 46:394-397(1995).
[7]
SEQUENCE OF 28-205 FROM N.A. (A*3004).
MEDLINE=9612443; PubMed=8560452;
Blaszczak R., Wehling J., Paessler M., Hahn U., Huhn D., Salama A.;
"A novel HLA-A30 allele (A*3004) identified by single-strand
conformation polymorphism analysis and confirmed by solid-phase
sequencing.";
Tissue Antigens 46:322-326(1995).
[8]
SEQUENCE OF 26-206 FROM N.A. (A*3006).
MEDLINE=20548605; PubMed=11098929;
Ellis J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H.,
Hurley C.K.;
"Diversity is demonstrated in class I HLA-A and HLA-B alleles in
Cameroon, Africa: description of HLA-A*03012, *2612, *3006 and HLA-
B*1403, *4016, *4703.";
Tissue Antigens 56:291-302(2000).
[9]
SEQUENCE OF 26-206 FROM N.A. (A*3007).
MEDLINE=20309230; PubMed=10852390;
Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester R.,
Ng J., Hartman R.J., Hurley C.K.;
"Seventeen more novel HLA-A locus alleles.";
Tissue Antigens 55:369-373(2000).
[10]
SEQUENCE FROM N.A. (A*3008).
MEDLINE=21108617; PubMed=11169261;
Cox S.T., McWhinnie A.J., Koester R.P., Heine U., Holman R.,
Madrigal A.J., Little A.-M.;
"Further diversity at HLA-A and -B loci identified in Afro-Caribbean
potential bone marrow donors.";
Tissue Antigens 57:70-72(2001).
-!- FUNCTION: Involved in the presentation of foreign antigens to
the immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of A-30 are known: A*3001
(A30.3), A*3002, A*3003, A*3004 (A30W7), A*3006, A*3007 and
A*3008. The sequence shown is that of A*3001.

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or send an email to license@isb-sib.ch).

EMBL; M30576; AAA59612.1; -
EMBL; U07234; AAA70162.1; -
EMBL; X61702; CAA43871.1; -
EMBL; M93657; AAA58650.1; -
EMBL; Z34921; CAA84401.1; -
EMBL; U19734; AAB53658.1; -
EMBL; U18988; AAB53658.1; JOINED.
EMBL; U24261; AAB50434.1; -
EMBL; X83770; CAA58723.1; -
EMBL; X83771; CAA58724.1; -
EMBL; AF028714; AAC14191.1; -
EMBL; AF028713; AAC14191.1; JOINED.
EMBL; AF065643; AAC18600.1; -
EMBL; AF065642; AAC18600.1; JOINED.
EMBL; AJ249308; CAB57306.1; -
EMBL; AJ249309; CAB57306.1; JOINED.
EMBL; AJ249310; CAB57306.1; JOINED.
EMBL; AJ249311; CAB57306.1; JOINED.
EMBL; AJ249312; CAB57306.1; JOINED.
EMBL; AJ249313; CAB57306.1; JOINED.
EMBL; AJ249314; CAB57306.1; JOINED.
EMBL; AJ249315; CAB57306.1; JOINED.
PIR; I38519; I38519.
PIR; I56039; I56039.
HSSP; Q95352; LHKK.
Genew; HGNC:4931; HLA-A.
MIM; 142800; -
GO; GO:0005887; C: integral to plasma membrane; NAS.
GO; GO:0030106; F: MHC class I receptor activity; NAS.
GO; GO:0006935; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR01039; MHC_I.
Pfam; PF00047; Ig; 1.
Pfam; PF0129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGcl; 1.
PROSITE; PS00835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC_I; Transmembrane; Glycoprotein; Signal; Polymorphism.

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FT SIGNAL 1 24
FT CHAIN 25 365
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT VARIANT 227 283
FT VARIANT 21 21
FT VARIANT 33 33
FT VARIANT 55 55
FT VARIANT 80 80
FT VARIANT 86 86
FT VARIANT 89 90
FT VARIANT 94 94
FT VARIANT 100 101
FT VARIANT 175 176
FT VARIANT 176 176
FT VARIANT 180 180
FT CONFLICT 33 33
FT SEQUENCE 365 AA; 40904 MW; 521166D95FBDC28 CRC64;

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Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGTFQKWAADVVPSEGEQRYTCHVQHEGLP 267
DB 248 QTQDTLVETRPAGDGTGTFQKWAADVVPSEGEQRYTCHVQHEGLP 291

RESULT 14
ID 1A36 HUMAN STANDARD; PRT; 365 AA.
AC P30455; QSMY89;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, A-36 alpha chain precursor
DE (MHC class I antigen A*36) (Aw-36).
DE HLA-A OR HLA.
CN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A. (A*3601).
RA Madrigal J.A., Balich M.P., Hildebrand W.H., Benjamin R.J.,
RA Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
RA Martell R.W., du Toit E.D., Parham P.;
RA "Distinctive HLA-A,B antigens of black populations formed by
RA interallelic conversion."
RA J. Immunol. 149:3411-3415(1992).
RA [2]
RA SEQUENCE OF 26-206 FROM N.A. (A*3602).
RA Rizzuto G.A., Hurley C.K.;
RA "Novel HLA-A Allele."
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC !- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC !- SUBCELLULAR LOCATION: Type I membrane protein.
CC !- POLYMORPHISM: The following alleles of A-36 are known: A*3601 and
CC A*3602. The sequence shown is that of A*3601.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; X61700; CA43869.1; -.
CC EMBL; AF274505; AAF78082.1; -.
CC EMBL; AF274504; AAF78082.1; JOINED.
CC PIR; I37478; I37478.
CC HSSP; 095352; 1HKH.
CC Genew; HGNC:4931; HLA-A.
CC MIM; 142800; .
CC GO; GO:0005887; C:integral to plasma membrane; NAS.
CC GO; GO:0030106; F:MHC class I receptor activity; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003597; IG_c1.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00447; IG; 1.
CC Pfam; PF00129; MHC_I; 1.
CC PRINTS; PR01638; MHCCLASSI.
CC ProDom; PD000050; MHC_I; 1.
CC SMART; SM00407; IGc1; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT TRANSMEM 333 365
FT DOMAIN 110 110
FT CARBOHYD 125 188
FT DISULFID 227 283
FT VARIANT 182 182
FT VARIANT 185 185
FT SEQUENCE 365 AA; 40934 MW; BA00A008598CD3E CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGTFQKWAADVVPSEGEQRYTCHVQHEGLP 267
DB 248 QTQDTLVETRPAGDGTGTFQKWAADVVPSEGEQRYTCHVQHEGLP 291

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:28:12 ; Search time 20 Seconds
(without alignments)
1317.824 Million cell updates/sec

Title: US-09-819-371-5
Perfect score: 274
Sequence: 1 GSHSLRFTAVSRPGRGEP.....QRYTCHVQHEGLPQLILRW 274

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 78:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	362	2 A60384	MHC class I histoc
2	126	46.0	345	2 S07114	MHC class I histoc
3	73	28.6	316	2 C37028	MHC class I histoc
4	59	21.5	348	2 S29990	histocompatibility
5	44	16.1	275	1 HLH10	MHC class I histoc
6	44	16.1	298	2 S44994	class I histocompa
7	44	16.1	313	2 I36958	MHC class I histoc
8	44	16.1	325	2 I54449	MHC class I histoc
9	44	16.1	332	2 S06424	MHC class I histoc
10	44	16.1	345	2 I68749	histocompatibility
11	44	16.1	354	2 I54551	MHC class I histoc
12	44	16.1	357	2 I36966	MHC class I protei
13	44	16.1	357	2 I36965	MHC class I histoc
14	44	16.1	359	1 HLH12	MHC class I histoc
15	44	16.1	364	2 S03535	class I histocompa
16	44	16.1	365	2 S77963	MHC class I histoc
17	44	16.1	365	2 I37476	MHC class I histoc
18	44	16.1	365	2 I37478	MHC class I histoc
19	44	16.1	365	2 S01171	class I histocompa
20	44	16.1	365	2 A47636	MHC class I histoc
21	44	16.1	365	2 I61856	MHC class I histoc
22	44	16.1	365	2 I83063	A11.2 - human
23	44	16.1	365	2 I36961	MHC class I protei
24	44	16.1	365	2 I54416	HLA-A*24 protein -
25	44	16.1	365	2 I38519	MHC class I histoc
26	44	16.1	365	2 I56039	HLA-A*30.3 precurs
27	44	16.1	365	2 I54493	MHC class I histoc
28	44	16.1	365	2 I38518	HLA-A*0102 allele
29	44	16.1	366	1 HLH0W3	MHC class I histoc

30	44	16.1	366	2 JS0262	class I histocompa
31	44	16.1	366	2 B37028	MHC class I histoc
32	44	16.1	366	2 S42823	MHC class I histoc
33	44	16.1	366	2 I37523	MHC class I histoc
34	44	16.1	366	2 JH0526	MHC class I histoc
35	44	16.1	366	2 I37527	MHC class I histoc
36	44	16.1	366	2 I72113	MHC histocompatibi
37	44	16.1	366	2 I38507	MHC class I histoc
38	44	16.1	366	2 I37526	MHC class I histoc
39	44	16.1	366	2 I61866	MHC class I histoc
40	44	16.1	366	2 I38505	MHC class I histoc
41	44	16.1	366	2 I68712	MHC class I histoc
42	44	16.1	366	2 I81231	lymphocyte antigen
43	44	16.1	366	2 I81232	lymphocyte antigen
44	44	16.1	366	2 I37544	MHC class I histoc
45	44	16.1	366	2 I37135	MHC class I histoc

ALIGNMENTS

RESULT 1

A60384
MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Jul-1999
C/Accession: A60384; JLO147
R/Lury, D.; Epstein, H.; Holmes, N.
Int. Immunol. 2, 531-537, 1990
A/Title: The human class I MHC gene HLA-F is expressed in lymphocytes.
A/Reference number: A60384; MUID:91197899; PMID:1707859
A/Accession: A60384
A/Molecule type: DNA
A/Residues: 1-362 <LUR>
R/Graghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.
J. Exp. Med. 171, 1-18, 1990
A/Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I
A/Reference number: JLO147; MUID:9011605; PMID:1688605
A/Accession: JLO147
A/Molecule type: DNA
A/Residues: 1-362 <GER>
A/Cross-references: GB:X17093; NID:G32223; PIDN:CAA34947.1; PID:G312407
A/Experimental source: Lymphoblastoid cell line
C/Genetics:
A/Gene: GDB:HLA-F
A/Cross-references: GDB:125714
A/Map position: 6p21.3-6p21.3
A/Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 362/1
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
C/Keywords: Glycoprotein; heterodimer; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-111/Domain: alpha-1 <A11>
F:78-104/Region: hypervariable
F:112-203/Domain: alpha-2 <AL2>
F:164-192/Region: hypervariable
F:204-235/Domain: alpha-3 <AL3>
F:217-282/Domain: immunoglobulin homology <IMM>
F:107/Binding site: carbohydrate (Asn) #status predicted

Query Match 100.0%; Score 274; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.3e-282;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GSHSLRFTAVSRPGRGEPRIAYEVDTQFLRSDDAIIRMEPRPWFQEGPOYW	60
Db	22	GSHSLRFTAVSRPGRGEPRIAYEVDTQFLRSDDAIIRMEPRPWFQEGPOYW	81
Qy	61	EWTTGYAKANAQTDRLVALRLRLRYNOSEAGSHTLQMGNGCDMGDPGRLLRGVHQHAYDG	120
Db	82	EWTTGYAKANAQTDRLVALRLRLRYNOSEAGSHTLQMGNGCDMGDPGRLLRGVHQHAYDG	141
Qy	121	KDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFTYLEGSCLELLRLRYLENGKETLQ	180